

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:20 ; Search time 47.9168 Seconds
(without alignments)
2698.100 Million cell updates/sec

Title: US-09-303-232-6
Perfect score: 2640
Sequence: 1 MAPMLAALALLPVPSEQ.....LFTIATVALLSAPHIIVQ 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapert 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriaph.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2640	100.0	501	Q9XZ14	Q9XZ14 heliothis v
2	2194	83.1	494	Q8T7S1	Q8T7S1 drosophila
3	2181	82.6	494	Q8T7S2	Q8T7S2 drosophila
4	2177	82.5	494	Q8T7S3	Q8T7S3 drosophila
5	2176.5	82.4	509	Q8T7S0	Q8T7S0 drosophila
6	2156.5	81.7	523	Q8T7R9	Q8T7R9 drosophila
7	1833	69.4	554	Q9VL79	Q9VL79 drosophila
8	1803.5	68.3	496	Q9XZ13	Q9XZ13 heliothis v
9	1800.5	68.2	807	Q8T7V5	Q8T7V5 drosophila
10	1786.5	67.7	545	Q9VM19	Q9VM19 drosophila
11	1705.5	64.6	525	Q8IP2	Q8IP2 drosophila
12	1258.5	47.7	502	Q9JHD6	Q9JHD6 mus musculus
13	1226.5	46.5	511	Q03481	Q03481 gallus gall
14	1145.5	43.4	480	Q81932	Q81932 caenorhabdi
15	1132	42.9	461	Q91197	Q91197 caenorhabdi
16	1124	42.6	273	Q9VJT9	Q9VJT9 drosophila

17	1085	41.1	554	5	062083	062083 caenorhabdi
18	1083.5	41.0	542	5	Q18556	Q18556 caenorhabdi
19	985	37.3	335	5	Q9NKD1	Q9NKD1 drosophila
20	982	37.2	537	5	Q8MUR0	Q8MUR0 apis mellif
21	978	37.0	515	5	Q46133	Q46133 locusta mig
22	973.5	36.9	537	5	Q9U941	Q9U941 myzus persi
23	970.5	36.8	499	11	Q8R4G9	Q8R4G9 mus musculu
24	970.5	36.8	504	11	Q8BV44	Q8BV44 mus musculu
25	966.5	36.6	499	11	Q8VHH6	Q8VHH6 mus musculu
26	964.5	36.5	567	5	Q9VC74	Q9VC74 drosophila
27	961	36.4	531	5	Q96632	Q96632 heliothis v
28	959.5	36.3	523	5	Q46128	Q46128 heliothis v
29	953.5	36.1	536	5	Q8T0Y9	Q8T0Y9 aplysia cal
30	951.5	36.0	552	5	Q91765	Q91765 myzus persi
31	951.5	36.0	568	5	Q9NFR5	Q9NFR5 drosophila
32	946.5	35.9	545	5	Q96631	Q96631 heliothis v
33	941	35.6	532	5	Q9U940	Q9U940 myzus persi
34	939.5	35.6	536	5	Q8T9S0	Q8T9S0 aplysia cal
35	939	35.6	533	5	Q8WRS1	Q8WRS1 chilo suppr
36	935	35.4	497	5	Q46135	Q46135 locusta mig
37	934	35.4	532	5	Q8MUB6	Q8MUB6 aphid gossy
38	932	35.3	494	11	Q8K0A7	Q8K0A7 mus musculu
39	930	35.2	595	5	Q91764	Q91764 myzus persi
40	926	35.1	494	11	Q9R0W9	Q9R0W9 mus musculu
41	920.5	34.9	496	6	Q8SPU6	Q8SPU6 bos taurus
42	920	34.8	517	5	Q96633	Q96633 heliothis v
43	918.5	34.8	512	11	Q91X60	Q91X60 mus musculu
44	917	34.7	452	13	Q918C7	Q918C7 gallus gall
45	916.5	34.7	495	11	Q8R493	Q8R493 mus musculu

ALIGNMENTS

RESULT 1

Q9XZ14 ID Q9XZ14 PRELIMINARY; PRT; 501 AA.
AC Q9XZ14;
DT 01-NOV-1999 (TREMREL. 12, Created)
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
DT 01-MAR-2003 (TREMREL. 23, Last annotation update)
DE Putative nicotinic acetylcholine receptor alpha 7-2 subunit.
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Noctuoidea;
OC Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte T., Oellers N., Adamczewski M.;
RT "Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than
to other insect nicotinic acetylcholine receptor alpha subunits.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF143847; AAD32698.1; -
DR InterPro: IPR006201; Neur_chan.
DR InterPro: IPR006202; Neur_chan_LBD.
DR InterPro: IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 501 AA; 56704 MW; 43CB0DC3960C78AB CRC64;

Query Match 100.0%; Score 2640; DB 5; Length 501;
Best Local Similarity 100.0%; Pred. No. 5.1e-240; Indels 0; Gaps 0;
Matches 501; Conservative 0; Mismatches 0;

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Qy 1 MAPLAALALLPVSEQGPHEKRLNALLANYNTLPRVANESPELEVRFGTLTQQII 60
Db 1 MAPLAALALLPVSEQGPHEKRLNALLANYNTLPRVANESPELEVRFGTLTQQII 60
Qy 61 DVDEKNOLLITNWLSEWYDNLRWNDSEYGGVKDLRITPNKLRKPDVLMYNSADGGFD 120
Db 61 DVDEKNOLLITNWLSEWYDNLRWNDSEYGGVKDLRITPNKLRKPDVLMYNSADGGFD 120
Qy 121 GTYQTNVVRSGSCLVPPGIFKSTCKMDIAWFPDDQDCHDMKFGSWTYDGNQLDLVK 180
Db 121 GTYQTNVVRSGSCLVPPGIFKSTCKMDIAWFPDDQDCHDMKFGSWTYDGNQLDLVK 180
Qy 181 DEAGDLSDFITNGEWYLGMPGKKNITTYACCPYVDVTFIMIRRTLYYFFNLIVP 240
Db 181 DEAGDLSDFITNGEWYLGMPGKKNITTYACCPYVDVTFIMIRRTLYYFFNLIVP 240
Qy 241 CVLSSWALLGFTLPPDSGEKLTGVTLLSLTVFLNLVAETLPOVSDAIPLLGTYFNCI 300
Db 241 CVLSSWALLGFTLPPDSGEKLTGVTLLSLTVFLNLVAETLPOVSDAIPLLGTYFNCI 300
Qy 301 MFVYASSVLTVVVLYNHHRTADITHMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMN 360
Db 301 MFVYASSVLTVVVLYNHHRTADITHMPQWIKSVFLQWLPWILRMSRPGKKITRKTIMN 360
Qy 361 TMRLELEKERSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFRRSFVR 420
Db 361 TMRLELEKERSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFRRSFVR 420
Qy 421 PSTMEDVGGGSHHRELHLILRELQFITARMKKADEAEELISDWKFAAMVVDRECLVFV 480
Db 421 PSTMEDVGGGSHHRELHLILRELQFITARMKKADEAEELISDWKFAAMVVDRECLVFV 480
Qy 481 TLFTIATVAVLLSAPHIIIVQ 501
Db 481 TLFTIATVAVLLSAPHIIIVQ 501

RESULT 2
Q8T7S1
ID Q8T7S1 PRELIMINARY; PRT; 494 AA.
AC Q8T7S1;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 23, last sequence update)
DE 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type III.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. PubMed=11973307;
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing."
RL Genetics 160:1519-1533(2002).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL; AF321447; AAM13394.1;
DR FlyBase; FBgn0032151; nACR-alpha-30D.
DR InterPro; IPR006201; Neur_chan_memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_LBD.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRfam; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;

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KW Transmembrane.
SQ SEQUENCE 494 AA; 56113 MW; 48327537229573FF CRC64;
Query Match 83.1%; Score 2194; DB 5; Length 494;
Best Local Similarity 82.6%; Pred. No. 5.7e-198;
Matches 418; Conservative 31; Mismatches 37; Indels 20; Gaps 3;
Qy 2 APLAALAL-----LALLPVSEQGPHEKRLNALLANYNTLPRVANESPELEVRFGTL 55
Db 3 SPLASLSFLVLLIFLAIRKESQGPHEKRLNALLANYNTLPRVANESPELEVRFGTL 62
Qy 56 LQIIDIYDEKNOLLITNWLSEWYDNLRWNDSEYGGVKDLRITPNKLRKPDVLMYNSA 115
Db 63 LQIIDIYDEKNOLLITNWLSEWYDNLRWNDSEYGGVKDLRITPNKLRKPDVLMYNSA 122
Qy 116 DEFGDGTQYNVVRSGSCLVPPGIFKSTCKMDIAWFPDDQDCHDMKFGSWTYDGNQL 175
Db 123 DEFGDGTQYNVVRSGSCLVPPGIFKSTCKMDIAWFPDDQDCHDMKFGSWTYDGNQL 182
Qy 176 DLVLKDRAGDLSDFITNGEWYLGMPGKKNITTYACCPYVDVTFIMIRRTLYYFF 235
Db 183 DLVLNSEDGDLSDFITNGEWYLLAMPKKNITTYACCPYVDITFIQIRRTLYYFF 242
Qy 236 NLIVPCVLISSMALLGFTLPPDSGEKLTGVTLLSLTVFLNLVAETLPOVSDAIPLLGT 295
Db 243 NLIVPCVLISSMALLGFTLPPDSGEKLTGVTLLSLTVFLNLVAETLPOVSDAIPLLGT 302
Qy 296 YFCIMEPMWASSVLTVVVLYNHHRTADITHMPQWIKSVFLQWLPWILRMSRPGKKITRK 355
Db 303 YFCIMEPMWASSVLTVVVLYNHHRTADITHMPQWIKSVFLQWLPWILRMSRPGKKITRK 362
Qy 356 TIMNTMRLELEKERSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFR 415
Db 363 TILLSNRKKELEKERSKSLANVLIDDDFRH-----TISGQTAIGSS----- 408
Qy 416 RSFVRPSTMEDVGGGSHHRELHLILRELQFITARMKKADEAEELISDWKFAAMVVDRE 475
Db 409 ASFGRTTVEEHTAICGNHKLHLILRELQFITARMKKADEAEELISDWKFAAMVVDRE 468
Qy 476 CLFVFTLTFTIATVAVLLSAPHIIIVQ 501
Db 469 CLIVFTLTFTIATVAVLLSAPHIIIVQ 494

RESULT 3
Q8T7S2
ID Q8T7S2 PRELIMINARY; PRT; 494 AA.
AC Q8T7S2;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, last annotation update)
DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type II.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A. PubMed=11973307;
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing."
RL Genetics 160:1519-1533(2002).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC EMBL; AF321446; AAM13393.1;
DR FlyBase; FBgn0032151; nACR-alpha-30D.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.

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RA Ceiniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.C., Brandon R.C., Rogers Y.,
RA Banazon J., An H., Baldwin D., Bazon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champs M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frick E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Housh J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,

Qy 418 FVRPSTMEDVGGLGSHHREHLHLRLRELQFTTARMKKADDEAEELISDWKFAAMVYDRFCL 477
 Db 423 GTHPSGDGP-----DLAKILEVRYIANFRCODESEVICSEWKFAACVDRCL 472
 Qy 478 FVFTLTFTIATVAVLLSAPHII 499
 Db 473 MAFSVFTICTIGILMSAPNFV 494
 RESULT 13
 Q03481
 ID Q03481 PRELIMINARY; PRT; 511 AA.
 AC Q03481;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Alpha8 subunit of nicotinic acetylcholine receptor precursor.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=90315158; PubMed=2369519;
 RX Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;
 RT "Brain alpha-bungarotoxin-binding protein cDNAs and mAbs reveal
 RT subtypes of this branch of the ligand-gated ion channel gene
 RT superfamily.";
 RL Neuron 5:35-48(1990).
 RC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 DR EMBL: X52296; CAA36544.1;
 DR InterPro: IPR006201; Neur_chanell.
 DR InterPro: IPR006202; Neur_chan_LBD.
 DR InterPro: IPR006029; Neur_chan_memb.
 DR Pfam: PF02931; Neur_chan_LBD; 1.
 DR Pfam: PF02932; Neur_chan_memb; 1.
 DR PRINTS: PR00252; NRIONCHANNEL.
 DR TIGRFS; TIGR00860; LIC; 1.
 DR PROSITE: PS00236; NEUOTR_ION_CHANNEL; 1.
 DR Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor; Signal;
 KW Transmembrane.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 511 POTENTIAL.
 SQ SEQUENCE 511 AA; 58705 MW; 10F362D153EC87A7 CRC64;
 Query Match 46.5%; Score 1226.5; DB 13; Length 511;
 Best Local Similarity 46.6%; Pred. No. 1e-106;
 Matches 246; Conservative 75; Mismatches 134; Indels 73; Gaps 9
 Qy 5 LAALALLALPVSEOGPEHKEKLLNALLANTLERPVANSEPLEVRFGLTLOQIIDVDE 64
 Db 16 LWASFLFFKVSQOGESQRRLYDLRNRLRPERVMNDSQPIVELQSLQLIIDVDE 75
 Qy 65 KNOLLITNLSLEWNDYNLRWNSYEGYVKDLRITPNKWKPDVLWYNSADGFGTYQ 124
 Db 76 KQVLITNANLQMTWVDIYLSWDQYEPGVQNLRFFSDQIWPFDILLYNSADERFDATFH 135
 Qy 125 TNVYVRSGGSLYPPGGIFKSTCKMDIAWFFDDQHCMDKFGSWTYDGNQLDLVLDKDEAG 184
 Db 136 TNVLVNSGSCQYIPPGILKSTCYIDVRWFFDVQKDLKFGSWTHGWLIDLQMLE--- 192
 Qy 195 GDLSDFTNGEWYLIQPGKKNITYACCEPVPVDVFTTMIARRTLTYFFNLIVPCVLI 244
 Db 193 ADISNYSINGEDWLVGPGKRNELYECCKEPPDVTTYITMRRTLYTGLNLLIPCVLI 252
 Qy 245 SSMAILGLTLPDPSGKILTLGVTLISLTVFLNLVAETLPQVSDATPLPLGTYFNCIMFW 304
 Db 253 SGCLAVLELLPADSGEKISLGITVLLSLTVMFLVLAETIMPATSDSVPLTAQFASIMVIV 312
 Qy 305 ASSVVLTVVVLNHYRTADIHMPQWTKSVFLOWLPMWILRMSRPGKKTKRKYIMNTRMR 364

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Db 313 GLSVVTVLVLPQHHDPOQAGKMPVWVRVILLNCAWFLRMKKGPGNI-----K 361
QY 365 ELELK-----ERSKSLANVLIDDDFRHGPPPPNSTASTGNL-----GPGCSIF 410
Db 362 PLSCKSYPKHHSLKNTENVL-----FCHQPSNGNMIIYSYHTMENPCC--- 406
QY 411 RTDFRRSFVRPSTMEDVGGGLG-----SHRELHL-----ILRELQFITAR 451
Db 407 -----PON-NDLGSKSGKITCPLSDNEHVKKALMDTIPVIVKILEEVQFTAMR 455
QY 452 MKKADAEALISDWKFAAMVVDRCLEVFILFIIATVAVLLSAPHII 499
Db 456 FRKQDEGEIECSEMKFAAAVIDRLCLVAFTLFAICTFTILMSAPNFI 503

RESULT 14
Q81932 PRELIMINARY; PRT; 480 AA.
AC Q81932;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DE Acetylcholine receptor protein 16, isoform b.
GN ACR-16.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA Waterston R.;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nelson J., Wohlmann P.;
RT "The sequence of C. elegans cosmid F25G6.";
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF022973; AAN84815.1;
KW Receptor.
SQ SEQUENCE 480 AA; 55274 MW; B5D6B707E50228A3 CRC64;

Query Match 43.4%; Score 1145.5; DB 5; Length 480;
Best Local Similarity 47.3%; Pred. No. 4.1e-99;
Matches 231; Conservative 71; Mismatches 135; Indels 51; Gaps 9;

QY 2 APLAALALLALPLVSPQGPHEKRLNALLANTLERPVANSEPLEVRLTLOQIID 61
Db 15 APTLGLS-----QERLYEDLMRNNLERPVANSEPVTVHLKVALQIID 61
QY 62 VDEKNOLLINILSWNDSEYGGVKKDLITPNKLNKPDVLMYNSADEGFDG 121
Db 62 VDEKNQVYVNAWLDYTWNDINLVMDKAEYGNITDVRFPAGIKWPKDVLVLYNSVDYTNFDS 121
QY 122 TYQTNVVRGGGLYVPPGIFKSTCKMDIAWPFDDQHKDMKFGSWTYDGNOLDLVLKD 181
Db 122 TYQTNMIVYTGVLVHWVPPGIFKISKIDITQWPFDDQKCFEFGSWTYDGYKLD--LQP 179
QY 182 EAGG-DLSDFITNGEWLYLGMGPKKNTIYACCPYVDVFTIMIRRRRLTYFFNLIVP 240
Db 180 ATGGFDISEVINGENALPLTTVERNEKFDCCPEPYDPVHFVLMRRRLTYGFLNIMP 239
QY 241 CVLISSMALGFTLPPDSGKELTGLVTILLSLVFLNLVAETLPOVSDAIPLLGTYFNCI 300

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Db 240 CILTTTLMTLGLFTLPDAGEKITLQITVLLSICFFLSIVSEMSPTTSEAVPLIGFTCC 299
QY 301 MFVASSVTVLVVLYNHHRTADIHENPOWIKSVFLQWLFPWILMRSPGKKITRKTII--M 358
Db 300 MIVVTASTVTVVLYNHHRTPTETHDGMPTWTRNLLLYWIPWILMRKRPNGHLYASLPSL 359
QY 359 MNTRMRELELKERSSKSLANVLID-----IDDFRHGPPPPNSTASTGNLGPCCS 408
Db 360 FSTK-----PNRHSSELRNIKDNEHLSRANSFDADCRNLQYIMTQSVSNGLTSLG-S 412
QY 409 IFTDFRRSFVRPSTMEDVGGGLGSHRE-----LHLLRELOFITARMKKADEAEALIS 463
Db 413 I-----PSTMISSNGTTTDSVQQATLLILHRIYHELKIVTKRMIEGDKREQACN 461
QY 464 DWKFAAMV 471
Db 462 NWKFAAMV 469

RESULT 15
P91197 PRELIMINARY; PRT; 461 AA.
AC P91197;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DE Hypothetical 52.7 kDa protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gattung S., Maggi L.;
RT "The sequence of C. elegans cosmid D2092.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; U88167; AAB42223.1;
DR WormPep; D2092.3; CE09102.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Hypothetical protein; Glycoprotein; Ionic channel;
KW Postsynaptic membrane; Transmembrane
SQ SEQUENCE 461 AA; 52718 MW; 6182A7F827357B92 CRC64;

Query Match 42.9%; Score 1132; DB 5; Length 461;
Best Local Similarity 44.7%; Pred. No. 7.2e-98;
Matches 216; Conservative 86; Mismatches 127; Indels 54; Gaps 6;

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QY. 23 EKRLNALLANVTNLRPVANSEPLEVRFGTLQOIIDVDEKNQLLITNIMLSLEWNDY 82
Db 26 ETKLTDLKGYNPLRPVQNSQPLEVKIKFLQOILDVDEKNQIVSVNAMLSTWFDH 85
QY 83 NLRWNDSEYGGVKDLRI--TPNKLWKPDLVLMYNSADEGFGDTYQTNNVVRSGSCLYVPP 140
Db 86 KIQWEPKYGGIQDIRPGSSDHIWKPDLVLLYNSAAEDFDTSNLLTYHTGTVVWIPP 145
QY 141 GIFKSTCKMDIAWFPDDQRCMDKFGSWYDGNQLDLVLKDEAGG----DLSDFITNGEW 196
Db 146 GVLKEVCQLDVTWFPDDQVCMDKFGSWFHGVAIDLQIDDDFTNGTQSMDLSTYLVNGEW 205
QY 197 YLIGMCKKNTITYACCPYVDVTFIMIRRTLYFFNLIVPCVLISSMALLGFTLPP 256
Db 206 QVISTNAKRVSVYKCCPEPYTVNYLHIRRTLYGFNLIIPLSLIISMAILGFMFPP 265
QY 257 DSGEKLTLGVTILLSTVFLNLVAETLPOVSDAIPLLGTYENCIMFMVASSVVLTVVVLN 316
Db 266 DAGEKITLEVITLLAIVFLSVSEWTPPTSEAVPLIGVFFSCCMLVVSASVVFTIVVLN 325
QY 317 YHRTADIIHEMPOWIKSVFLOLWPILRMSRPGKKITRKTIMNTRMRELELKERSSKL 376
Db 326 LHFRSADSHENPLVRRVLEFLPWLLFMSRPGYKFKV-----PSN----- 363
QY 377 LANVLDDDDFRHGPPPNSTASTGNLPGCCSIFRTDFRRSFVRPSTMEDVGGGLSHHR 436
Db 364 -ANVIDSTDKMPKKPNPLD-----CNL-----PSN-----HAGYEAQIL 397
QY 437 ELHLILRELOFITARKKKADEAEELISDNKFAAMVVDRCFLFVFTLTITATVAVLLSAP 496
Db 398 LLSHVTELRVVAVFYNKKEHDERIOTDRFAAMVVDRACLLFTVTVISILAINMSAP 457
QY 497 HII 499
Db 458 HII 460
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Search completed: August 13, 2003, 15:29:11
Job time : 49.9168 secs

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50. 305

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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:55 ; Search time 10.4907 Seconds
(without alignments)
2245.843 Million cell updates/sec

Title: US-09-303-232-6
Perfect score: 2640
Sequence: 1 MAPMLAALALLPVSEOG.....LFTIATVALLSAPHIIVO 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1258.5	47.7	502	1	ACH7_HUMAN
2	1255.5	47.6	502	1	ACH7_MOUSE
3	1253	47.5	502	1	ACH7_CHICK
4	1246.5	47.2	502	1	ACH7_RAT
5	1240.5	47.0	499	1	ACH7_BOVIN
6	1237.5	46.9	498	1	ACH1_CAEEL
7	989.5	37.5	503	1	ACH3_HUMAN
8	977.5	37.0	499	1	ACH3_RAT
9	970.5	36.8	495	1	ACH3_BOVIN
10	964.5	36.5	567	1	ACH1_DROME
11	948.5	35.9	496	1	ACH3_CHICK
12	946.5	35.9	516	1	ACH1_MANSE
13	944	35.8	557	1	ACH1_SCHGR
14	943	35.7	576	1	ACH2_DROME
15	933	35.3	494	1	ACH6_HUMAN
16	924.5	35.0	528	1	ACH2_CHICK
17	922.5	34.9	529	1	ACH2_HUMAN
18	919.5	34.8	512	1	ACH3_CARAU
19	917	34.7	511	1	ACH2_RAT
20	915.5	34.7	494	1	ACH6_CHICK
21	914.5	34.6	493	1	ACH6_RAT
22	910.5	34.5	495	1	ACHP_RAT
23	908.5	34.4	519	1	ACH4_DROME
24	906	34.3	457	1	ACHA_BOVIN
25	900	34.1	521	1	ACH3_DROME
26	899.5	34.1	500	1	ACHN_RAT
27	897.5	34.0	627	1	ACH4_HUMAN
28	896	33.9	456	1	ACHA_CHICK
29	895	33.9	502	1	ACHN_HUMAN
30	891	33.8	622	1	ACH4_CHICK
31	890	33.7	457	1	ACHA_RAT
32	890	33.7	470	1	ACHP_CHICK
33	887	33.6	498	1	ACHP_HUMAN

RESULT 1

ID	ACH7_HUMAN	STANDARD;	PRT;	502 AA.
AC	P36544; Q15826; Q96RH2; Q99555; Q9BXH0;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Neuronal acetylcholine receptor protein, alpha-7 chain precursor.			
GN	CHRNA7 OR NACHRA7.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=94195283; PubMed=8145738;			
RA	Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;			
RT	Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from the SH-SY5Y cell line and determination of pharmacological properties of native receptors and functional alpha 7 homomers expressed in Xenopus oocytes.;			
RT	Mol. Pharmacol. 45:546-554(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hippocampus;			
RA	Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;			
RL	Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97062879; PubMed=8906617;			
RA	Elliot K.J., Ellis S.B., Berckman K.J., Urrutia A., Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;			
RT	Comparative structure of human neuronal alpha 2-alpha 7 and beta 2-beta 4 nicotinic acetylcholine receptor subunits and functional expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and beta 4 subunits.;			
RT	J. Mol. Neurosci. 7:217-228(1996).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=97162233; PubMed=9009220;			
RA	Groot Kormelink P.J., Luyten W.H.M.L.;			
RT	"Cloning and sequence of full-length cDNAs encoding the human neuronal nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and expression of seven nAChR subunits in the human neuroblastoma cell line SH-SY5Y and/or IMR-32.;"			
RT	FEBS Lett. 400:309-314(1997).			
RN	[5]			
RP	REVISIONS.			
RA	Groot Kormelink P.J., Luyten W.H.M.L.;			
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Epidermal keratinocytes;			
RA	Arredondo J., Grando S.A.;			
RT	"Cloning cholinergic receptors in human keratinocytes.;"			

P04756 mus musculu
P19370 carassius a
P02708 homo sapien
P02711 torpedo mar
P09483 rattus norv
P09484 gallus gall
P02710 xenopus cal
P05377 xenopus lae
P22456 xenopus lae
P45963 caenorhabdi
Q98880 brachydanio
P18257 carassius a

ALIGNMENTS

Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [7]
 RN SEQUENCE OF 17-502 FROM N.A.
 RP TISSUE=Brain;
 RC Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
 RA Lee J., Tian J., Giordano T.;
 RT "Cloning and sequence of the human $\alpha 7$ nicotinic acetylcholine
 receptor.";
 RL Drug Dev. Res. 30:252-256(1993).
 RN [8]
 RP SEQUENCE OF 24-502 FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE=94245214; PubMed=8189270;
 RA Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretta M.,
 RA Heinemann S.F.;
 RT "Molecular cloning and chromosomal localization of the human $\alpha 7$ -
 nicotinic receptor subunit gene (CHRNA7).";
 RL Genomics 19:379-381(1994).
 RN [9]
 RP SEQUENCE OF 118-129 FROM N.A.
 RX MEDLINE=21818878; PubMed=11829490;
 RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
 RT "A 3-Mb map of a large segmental duplication overlapping the $\alpha 7$ -
 nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
 RL Genomics 79:197-209(2002).
 RN [10]
 RP MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE=21829512; PubMed=11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 protein expression map database.";
 RL Proteomics 2:212-223(2002).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- MASS SPECTROMETRY: MW=54157.68; METHOD=WALDI.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC
 DR EMBL; X70297; CAA49778.1; -
 DR EMBL; U40583; AAB3561.1; -
 DR EMBL; U62436; AAB4014.1; -
 DR EMBL; Y08420; CAA69697.1; -
 DR EMBL; AF385585; AAK68111.1; -
 DR EMBL; L25827; -; NOT ANNOTATED_CDS.
 DR EMBL; Z23141; CAA80672.1; -
 DR EMBL; AF332758; AAK19515.1; -
 DR PIR; G02259; G02259.
 DR PIR; I37185; ACHUA7.
 DR Genew; HGNC:1960; CHRNA7.
 DR MIM; 118511; -
 DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. .; TAS.
 DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. .; TAS.
 DR GO; GO:0000187; P:activation of MAPK; TAS.
 DR GO; GO:0006832; P:small molecule transport; TAS.
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neu_chan_LBD.
 DR InterPro; IPR006201; Neu_channel.

DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR PRINTS; PR00232; Neur_chan_memb; 1.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 22 BY SIMILARITY.
 FT CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT DOMAIN 23 230 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 231 255 POTENTIAL.
 FT TRANSMEM 262 280 POTENTIAL.
 FT TRANSMEM 296 317 POTENTIAL.
 FT DOMAIN 318 469 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 470 490 POTENTIAL.
 FT DISULFID 150 164 BY SIMILARITY.
 FT DISULFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 11 11 A -> G (IN REF. 1 AND 7).
 FT CONFLICT 58 58 S -> N (IN REF. 2 AND 6).
 FT CONFLICT 134 134 S -> P (IN REF. 2 AND 6).
 FT CONFLICT 364 364 C -> S (IN REF. 8).
 FT CONFLICT 375 375 A -> G (IN REF. 1).
 FT CONFLICT 409 413 RMACS -> AWPAP (IN REF. 8).
 SQ SEQUENCE 502 AA; 56449 MW; D94B3A482EAA0E42 CRC64;
 Query Match 47.7%; Score 1258.5; DB 1; Length 502;
 Best Local Similarity 48.68; Pred. No. 1.4e-103;
 Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;
 QY 8 LALLA-LLPYSEQPHKEKRLNALLNLYLERPVANSEPLEVRFGLTIQIIVDEKN 66
 DB 10 LALAASLLHVSLOGEFQKLYKLVKNYPLERPVANDSQPLTVYFSLSLQIMDVDEKN 69
 QY 67 QLLITNWLSELDWYNDYLRNDSEYGGVKDLRTPNKWKPDVLYMNASDEGDTGTQTN 126
 DB 70 QVLTNTNWLQMSWTQHYLQNVSEYPGVKTVRPGDGOIKWPKDILLYNSADERFATPHN 129
 QY 127 VVVRSGGCLYVPPGIFKSKCKMDIAWPFDDQHCMDKFGSWTYDGNQLDLVLKDEAGD 186
 DB 130 VLVNSSHCQYLPFGIFKSSCYIDVRFDPDVQHCCLKFGWSYGGWSLDLQME---AD 186
 QY 187 LSDFITNGEYLIGMPGKNTITYACCPYVDVFTTMRRTLYFFNLIVPCVLISS 246
 DB 187 ISGVIPNGEWDVIGPKGRSERFVECKPEYDVTFTVTRRTLYGLNLLIPCVLISA 246
 QY 247 MALLGFTLPDPSGEKLTGLVTLISLTVFLNVAETLPQVSDATPLGLGVFNCIMFVAS 306
 DB 247 LALLVFLPADSGEKISLGTITVLLSLTVFMLLVAEIMPATSDSVPLTQAQFASTMIIVGL 306
 QY 307 SVTLTVVVLNTHHRTADIHEMPQIKSVFQLQWLPWILMRSPRKKITRKITMMNTRREL 366
 DB 307 SVVTVTVLVQYHHDDPGGKMKPWTRVILLNWCANFLRMKRPGEKVPACQHKQRCSL 366
 QY 367 ELKERSKSLANVLDIDDDFRHGPPPNSTASTGNL-----GPGC 407
 DB 367 ASVEMSAVA-----PPP---ASGNLLYIGFRGLDGVHCVPTPDGSGVVC 407
 QY 408 SIFRTDFRSFVRPSTMEDV---GGGLSHHRLHLILRELQFITARKMKADEAEELISDW 465
 DB 408 G-----RMACSPHDEHLHGQPPGEGDPAKILLEVRYIANRFRQCDESEAVCSEW 460
 QY 466 KFAAMVDRFCFLVFTLTFTTIATVAVLSAPHII 499
 DB 461 KFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494
 RESULT 2
 ACH7_MOUSE

10	LALAAALLHVS	LQGEFFORRLYKELKNNYNPLERP	VANDSQBLTVYFSLSLQIMD	VDKNN 69
67	QLLITNTIWL	SLSEWNDYLNLRWDSYGGVKOLRITP	NKLNKLPDVLNMSADEGFGTYQTN	126
70	QVLTTNLQMS	WTDHYLQNNMSEYPGVKNYRFPDQ	GIWKPDILLYNSADERDATEFTN	129
127	VVVRSGGSLY	VVPGIPIKSTCKMDIANFPDDQHC	DMKFGSWTYDGNQLDLVLKDEAGD	186
130	VLVNASHCOY	LPPIEFKSSCYIDVRWFPDVOQC	KLKFGSWSGWSLQLQMQE---AD	186
187	LSDFITNGE	WYLIGMPCGKKNITTYACCPYVDVT	ITIMIRRTLYYFNLIVPCVLSS	246
187	ISSITNGE	MDLMPGKRNKEFYECCKEPPDVTY	VTMRRRTLYGLNLLIPCVLISA	246
247	MALIGFLTP	PDSPGSEKLTGLVITLLSLTVFLN	VAETLPQVSDAIPLLGTYFNCIMF	306
247	LALLVFLP	ADSGEKISLIGITVLLSLTVFMLV	AEIMPATSDSVPLIAQYFASITMI	306
307	SVVLTVVVL	NYNHHRTADIHMPQWIKSVFLO	WLPMILRMSRPGKKITRKTIMMNT	366
307	SVVTVTVL	RYHHHDPDGGKMPKWTIRILLN	WCAMFLRMKRPGEKVRPACQHK	PRRCSL 366
367	ELKERS-	---KSLLANVLDIDDDFR----	HGPPPNSTASTGNLPGCCSIFRT	DFRRS 417
367	ASVELS	SAGAPPTSTNGNLXYT--GFR	LEGMHCAPTDPSGVVCGRL--	ACSPTHDEHLMH 422
418	FVPSPTMED	VGGGLGSHHRELHLILRELQFT	ITARMKKADEAEALISDMKFAAM	VYDRFCL 477
423	GTHPSDGP	-----DLAKILEEVRYTANFR	CODESEVICSEWKFAACVYDR	LCJL 472
478	FVFTLFTI	ATVAVLLSAPHII 499		
473	MAFSVFTI	ICTIGILMSAPNEV 494		

RESULT 3

ACHT7_CHICK	STANDARD;	PRT;	502 AA.
ID	ACH7_CHICK		
AD	P22770;		
DT	01-AUG-1991 (Rel. 19, Created)		
DT	01-AUG-1991 (Rel. 19, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Neuronal acetylcholine receptor protein, alpha-7 chain precursor.		
OS	Gallus gallus (Chicken).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;		
OC	Gallus.		
OX	NCBI_TaxID=9031;		
ON	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RC	MEDLINE=91097796; PubMed=1702646;		
RX	Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S.,		
RA	Miller N., Valera S., Barkas T., Ballivet M.;		
RT	"A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is		
RT	developmentally regulated and forms a homo-oligomeric channel blocked		
RT	by alpha-BTX.";		
RL	Neuron 5:847-856(1990).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Brain;		
RC	MEDLINE=93015158; PubMed=2369519;		
RX	Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;		
RT	"Brain alpha-bungarotoxin binding protein cDNAs and WABs reveal		
RT	subtypes of this branch of the ligand-gated ion channel gene		
RT	superfamily.";		
RL	Neuron 5:35-48(1990).		
RN	[3]		
RP	SEQUENCE OF 1-18 FROM N.A.		
RC	STRAIN=White leghorn; TISSUE=Erythrocyte;		
RX	MEDLINE=93049204; PubMed=1425587;		
RA	Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M.,		
RA	Matter J.M.;		

RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor.
 promoter develops during morphogenesis of the central nervous
 system.";
 RT EMBO J. 11:4529-4538(1992).
 RN [4]
 RP SEQUENCE OF 24-47.
 RC TISSUE=Brain;
 RX MEDLINE=85270494; PubMed=3860855;
 RA Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
 Ray N., Raftery M.A.;
 RT "Brain and muscle nicotinic acetylcholine receptors are different but
 homologous proteins.";
 RT Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
 RL [5]
 RN MUTAGENESIS OF LEU-270.
 RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
 RX MEDLINE=93024917; PubMed=1383829;
 RA Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
 Hussy N., Bertrand S., Ballivet M., Changeux J.-P.;
 RT "Mutations in the channel domain alter desensitization of a neuronal
 nicotinic receptor.";
 RL Nature 353:846-849(1991).
 RN [6]
 RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
 RX MEDLINE=93024917; PubMed=1383829;
 RA Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
 Hussy N., Bertrand S., Ballivet M., Changeux J.-P.;
 RT "Mutations in the channel domain of a neuronal nicotinic receptor
 convert ion selectivity from cationic to anionic.";
 RL Nature 359:500-505(1992).

CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 MEMBRANE.
 CC -1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
 IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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CC EMBL; X52295; CAA36543.1; -;
 DR EMBL; X68246; CAA48317.1; -;
 DR EMBL; X68586; CAA48576.1; -;
 DR PIR; JN0113; JN0113.
 DR PDB; 1K4; 17-APR-02.
 DR PDB; 1K4; 17-APR-02.
 DR InterPro; IPR006029; Neu_channel_memb.
 DR InterPro; IPR006029; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRfams; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEURCTR_ION_CHANNEL; 1.
 KW postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT DOMAIN 24 230
 FT TRANSMEM 231 255
 FT TRANSMEM 262 280
 FT TRANSMEM 296 317
 FT DOMAIN 318 469 CYTOPLASMIC.

FT TRANSMEM 470 490
 FT DISULFID 150 164
 FT DISULFID 212 213
 FT
 FT CARBOHYD 46 46
 FT CARBOHYD 90 90
 FT CARBOHYD 133 133
 FT MUTAGEN 270 270
 FT
 FT CONFLICT 26 27
 FT SEQUENCE 502 AA; 56946 MW; 57325D4309AD2FD CRC64;
 Query Match 47.5%; Score 1253; DB 1; Length 502;
 Best Local Similarity 48.8%; Pred. No. 4.2e-103;
 Matches 250; Conservative 81; Mismatches 145; Indels 36; Gaps 8;
 QY 2 APLAALALLALLPVSEOGPEKRLNALLNANTYLERPVANSEPLEVFLGLTLOQIID 61
 DB 5 ALMLWLLAAGLVRESLQGEFQKLYKELLKNYPLRPVANDSQPLTVYFTLSLQIMD 64
 QY 62 VDEKNQLLTITNWLSEWNDYINLRWNSDEYGVKDKLRITPNKMLKPDVLMYNSADEGFDG 121
 DB 65 VDEKNQVLTITNWLQMYTQDHYLQWNVSEYGVKNVRFDPGLIWKPDILLYNSADERFA 124
 QY 122 TYOTNVVVRSGGSLYVPGIFKSTCKMDIAWTFDDQHCMDKFGSWTYDGNQLDLVLKD 181
 DB 125 TFHTNVLVNSGHCQYLPFGIFKSSCYIDVRWFFDVQKCNLKFSGWYGGWSLDQMQE 184
 QY 182 EAGDGLSDFITNGEWYLGMPGKNTITYACCPPEYVDVFTIMRRRTLYFFNLIVPC 241
 DB 185 ---ADISGYISNGEWDLVGPGRKTESFYECCKEYPDIFTVTMRRTLYGLNLLIPC 241
 QY 242 VLISALLGFTLPPDSEKLTGLVTLLSLTVFLNLVAETLPQVSDAIPLLGLTYFNCIM 301
 DB 242 VLISALLVFLPADSGEKISLITVLLSILTVFLNLVAETLPQVSDAIPLLGLTYFNCIM 301
 QY 302 FMVASSVVLTVVNLNHHRTADITHMPQWIKSVFLQWLPWILNRSRGGKTKTRTIMNT 361
 DB 302 IIVGLSVVTVIVLYVHHDPDGGKMPKWTIRILLNWCAMFLRMKRGEDKVRPACQHKQ 361
 QY 362 RMRELEKRSKSS---LLANVLIDIDDFR---HGPPPPNSTASTGLPGCSIFRT 412
 DB 362 RRCSLSSMENVTVSGQCSNGNMLYI---GFGLDGVHCTPTDTSVVICGRM--TCS--- 413
 QY 413 DFRSRFVRPSTMEDVGGGLSGSH---RELHLILRELQFITARKKKADEAEELISQWKF 467
 DB 414 -----PTEENL---LHSGHPSEGDPLAKILEEVRYIANFRDQDEEAICNWK 462
 QY 468 AAMVVDRECLFVFTLFTIATVALLSAPHII 499
 DB 463 AASVVDRLCLMAFSVFTIICITIGILMSAPNFV 494

RESULT 4

ACH7_RAT ID ACH7_RAT STANDARD; PRT; 502 AA.
 AC Q05941;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 GN CHRNA7 OR ACRN7.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93147931; PubMed=7678857;
 RA Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
 RT "Molecular cloning, functional properties, and distribution of rat
 brain alpha 7: a nicotinic cation channel highly permeable to

127	VVRSGGSCLYVPPIGIFKSTCKMDIAWFPDDQHCNMKGSGWTYDGNQLDLVLKDAGGD	186
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
130	VLVNASGHCOYLPGIEFKSCTIDVRWFDPDOCKLKFSGWSYGLDLOMQE----	AD 186
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
187	LSDFITNGEWYLGMPGKKNTIYACCPDYVDVTFTIMRRRTTYFFNLIVPCVLIS	246
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
187	ISSYPINGEDMLGIPGRKEKFEYCEKPEYDVTVTVMRRRTTYGLNLLIPCVLISA	246
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
247	MALLGFTLPDPSGEKLGTVITILLSLVFNLVLAETLPQVSDAIPLLTGYFNCINEMVAS	306
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
247	LALLVFLPADSGEKISLGITVLLSVFMLLVAETIMPATDSVPLIAQYFASTMIIVL	306
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
307	SVLTVVVLNYHHRDATIHEMPQIKSVFLQWLPIWRMRPCKKITRKTIMMTRMREL	366
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
307	SVVTVIVLRHHHPDGGMKPWKTRIILLNWCAFWELRMKRPGCDKVRPAQHKKPRCSL	366
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
367	EKKERS-----KSLLANVLDDDDR-----HGPPPNPNSTASTGNLGPCCSIPTDFRS	417
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
367	ASVELSAGAPPTSNGNLLYI--GFRLGEMHCAPTDSGVVCGRL--ACSPTHDEHLMH	422
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
418	FVRESTMEDVGGLSHRHRELHLILRELQFIITARMKKADEAEALISDWKFAAMVDRFCL	472
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
423	GAHSDGDP-----DLAKILEEVRIANRNCRQDESEVICSEWFAACVDPDLCL	472
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
478	FVTLFTTIATVAVLLSAPII 499	
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
473	MAFSVETICTIGILMSAPNFV 494	
I:	: I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I : I :	:
<hr/>		
RESULT 5		
ACH7_BOVIN		
ID	ACH7_BOVIN STANDARD; PRT; 499 AA.	
P54131;		
01-OCT-1996 (Rel. 34, Created)		
01-OCT-1996 (Rel. 34, Last sequence update)		
28-FEB-2003 (Rel. 41, Last annotation update)		
Neuronal acetylcholine receptor protein, alpha-7 chain precursor. CHRNA7.		
Bos taurus (Bovine).		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.		
NCBI_TaxId=9913;		
[1]		
SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).		
TISSUE=Adrenal medulla;		
MEDLINE=95346009; PubMed=7620615;		
Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W., Gutierrez L., Criado M.;		
"Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine chromaffin cells: molecular cloning, functional expression and alternative splicing of the alpha 7 subunit.";		
Eur. J. Neurosci. 7:647-655(1995).		
-! FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA MEMBRANE.		
-! SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA- BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY SIMILARITY). HOMO-OLIGOMER OF THE SHORT FORM GIVES RISE TO UNFUNCTIONAL CHANNELS, AS DOES COEXPRESSION OF BOTH LONG AND SHORT FORMS OF THE RECEPTOR.		
-! SUBCELLULAR LOCATION: Integral membrane protein.		
-! ALTERNATIVE PRODUCTS: Event-Alternative splicing; Named isoforms=2; Name=Long; IsoId=P54131-1; Sequence=Displayed; Name=Short; IsoId=P54131-2; Sequence=VSP_000075;		
-! TISSUE SPECIFICITY: AT LEAST IN CHROMAFFIN CELLS.		
-! SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.		

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CC -----
 CC EMBL; X93604; CAA63802.1; .
 DR InterPro: IPR006029; Neu_chan_memb.
 DR InterPro: IPR006202; Neur_chan_LBD.
 DR InterPro: IPR006201; Neur_chan.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 499
 FT
 FT DOMAIN 20 227
 FT TRANSMEM 228 252
 FT TRANSMEM 259 277
 FT TRANSMEM 293 314
 FT DOMAIN 315 466
 FT TRANSMEM 467 487
 FT DISULFID 147 161
 FT DISULFID 209 210
 FT
 FT CARBOHYD 43 43
 FT CARBOHYD 87 87
 FT CARBOHYD 130 130
 FT VARSPLIC 262 290
 FT
 FT SEQUENCE 499 AA; 56002 MW; AEE50B3820D42D5 CRC64;
 Query Match 47.0%; Score 1240.5; DB 1; Length 499;
 Best Local Similarity 49.4%; Pred. No. 5.3e-102;
 Matches 247; Conservative 78; Mismatches 152; Indels 23; Gaps 6;

QY 8 LALLA-LLPVSEQPEKRLNALLNANTLERPVANSEPLEVRFGTLTQIIVDDEKN 66
 DB 7 LALAASLHLSVGEFORKLYKLVKNYNLERPVANDSLPLVYFSLSLQIIVDDEKN 66
 QY 67 QLLITNLSLEWNYDLNRNDSYGGVKKDLRITPNKLRKPDVLMYNSADEGFGTYQTN 126
 DB 67 QVLTNTNLQMTDHYLQWNASSEYCGVKTVPDPDGOIKWPKDILLYNSADERFATPHN 126
 QY 127 VVVRSGGSLVPPGIFKSTCKMDIANFPDDQDCKMFGSWYDGNQLDLVLDKDEAGD 186
 DB 127 VLVNSSGHCQYLPPIGIFKSSYIDVRFPDVOQCKLFGSWYGGWSLDQWQE---AD 183
 QY 187 LSDFITNGEWYLGMPCKNTITVACCPVVDVFTIMIRRRRTLYFFNVLVPCVLISS 246
 DB 184 ISGYPNGEMDLVGLGRSEKFEYCKEYPPDVTFTVSRRTLYGLNLLIPCVLISA 243
 QY 247 MALLGFTLPDPSGKELTGLVITLLSLAVFLNLVAETLPOVSDAIPLLGTYFNCIMFVAS 306
 DB 244 LALLVFLPADSGEKISGLITVLLSLVFMLLVAEIMPATSDSVPLIAQVFASTMIIVGL 303
 QY 307 SVVLTVVVYVYHHTADIEHMPQWIKSVFLQWLPWILRMSRPGKIKTKIMNTRREL 366
 DB 304 SVVTVIVLQYHHDPDGGKMPKTRVYVLLNWCWAFMRMKRPGDKYRPAQOHNRCSL 363
 QY 367 ELKERS--KSLANVLDDDD--DFRHGPPPPNSTASTGNLPGCKSIFRTDFRRSFV 419
 DB 364 ASVMSAVAGPPATNGNLLYTGFLDTHMCAPTDSGVVCGRV--ACSPHDEHLLHAG 421
 QY 420 RPSTMEDVGGGLGSHHRLHLILRELQFITARMKKADEAEELISDWKFAAMVDFCLFV 479
 DB 422 QPSEGD-----DLAKILEVRYIAHFRFCQDESEAVCFACVVDRLCLMA 471

QY 480 FTLFTIATVAVLLSAPHII 499
 DB 472 FSVFTILCTIGILMSAPNV 491
 RESULT 6
 ACHI_CAEEL STANDARD; PRT; 498 AA.
 ID ACHI_CAEEL
 AC P48180;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor like protein, alpha-type chain precursor.
 GN F25G6.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=96196478; PubMed=8627624;
 RA Ballivet M., Alliod C., Bertrand S., Bertrand D.;
 RT "Nicotinic acetylcholine receptors in the nematode Caenorhabditis
 RT elegans".
 RL J. Mol. Biol. 258:261-269(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Nelson J., Wohldmann P.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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CC -----
 CC EMBL; X83887; CAA58764.1; .
 DR EMBL; AF022973; AAC25796.1; .
 DR PIR; S68588; S68588.
 DR HSP; P58154; I19B.
 DR WormPep; F25G6.3; CE09639.
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_chan.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
 KW Transmembrane; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 498
 FT
 FT DOMAIN 20 230
 FT TRANSMEM 231 252
 FT TRANSMEM 261 279
 FT TRANSMEM 295 314
 FT DOMAIN 315 472
 FT TRANSMEM 473 493
 FT DISULFID 147 161
 FT DISULFID 211 212
 FT
 FT CARBOHYD 43 43
 FT CARBOHYD 93 93
 FT
 FT ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
 FT ALPHA-TYPE CHAIN.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT POTENTIAL.
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT POTENTIAL.
 FT BY SIMILARITY.
 FT ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 498 AA: 57169 MW; E463ABB40AC9FA82 CRC64;

Query Match 46.9%; Score 1237.5; DB 1; Length 498;
 Best Local Similarity 47.5%; Pred. No. 9,7e-102;
 Matches 245; Conservative 80; Mismatches 140; Indels 51; Gaps 9;

QY 2 APMALALALLPVSQEPHEKRLNALLANYTLRPNVANESEPLEVRFGLTQQIID 61
 DB 15 APTAGSL-----QERRLYEDLMRYNNLRLRPVANHSEPTVHLKVALQQIID 61

QY 62 VDEKNOLLITNIWLSLEWYDNLRWNSYGVGKDLRITPNKLPKPDVLWYNSADGPDG 121
 DB 62 VDEKQVYVYVNAWLDYTWNDYVNDWAKAEGNITDVRFPAGIKWPDVLLYVNSVDTFDS 121

QY 122 TYQTNVVRSGSCLYVPPGIFKSTCKMDIAFPDDQHCMDKFGSWTYDGNQLDLVLKD 181
 DB 122 TYQTNMIVSTGLVHWVPPGIFKISKIDIQWFPDDEQKCFKFGSWTYDGVKLD--LQp 179

QY 182 EAGG-DLSDFINGEWLGMGPKKNTIYACCPYVDVTFIMIRRTLYFFNLIVP 240
 DB 180 ATGGFDISEYISNGEWALPLTTVERNEKFDCCPEYDPVDFHFLMRRTLYYGFNLIMP 239

QY 241 CVLISSMALLGTLPPDSEKTLGVTILLSTVFLNLVAETLPQVSDAIPLLGYENCI 300
 DB 240 CILTILMLUGTLPPDAGEKITLQITVLSICFLSIVSEMSPTSEAVPLLGIFFTCC 299

QY 301 MPMVASSVYLVVLYNHRHTADIHEMPQWIKSVFLOWLPWILRMRPGKTKIRTKI--M 358
 DB 300 MIWVTASTVTVVVLNLHVRTPETHDMGPWTRNLLLYWIPWILRMRPGHNLTYASLPSL 359

QY 359 MNTRELEKERSKSLLANVLD-----IDDFRHGPPPPNPNSTASTGNLPGGCS 408
 DB 360 FSTK-----PNRHSLSLRNKDNEHSLSRANSFADACRLNQYIMTQSVNSGLTSLG-S 412

QY 409 IFTDFRRSEFVSPSTMEDVGGGLSGSHRE-----LHLILRELQFTIARMKKADEAELIS 463
 DB 413 I-----PSTMISSNGTTDVSQQTLLILHRYHLEKIYTKRMIEGDKKEQACN 461

QY 464 DNKFAAMVVDRLCFVFTLFTIATIAVALLSAPHII 499
 DB 462 NKKFAAMVVDRLCLVFTIFIVSTIGIPWSAPYLV 497

RESULT 7
 ACH3_HUMAN
 ID STANDARD; PRT: 503 AA.
 AC P32297; Q15823; Q96RH3; Q95553; Q9BQ93;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
 GN CHRNA3 OR NACHRA3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90245296; PubMed=2336208;
 RA Fornasari D., Chini B., Taroni P., Clementi F.;
 RT "Molecular cloning of human neuronal nicotinic receptor alpha
 RT 3-subunit";
 RL Neurosci. Lett. 111:351-356(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thymus;
 RX MEDLINE=91114756; PubMed=1989896;
 RA Mihovilovic M., Roses A.D.;
 RT "Expression of mRNAs in human thymus coding for the alpha 3 subunit
 RT of a neuronal acetylcholine receptor";
 RL Exp. Neurol. 111:175-180(1991).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=97062879; PubMed=8906617;
 RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
 RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
 RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
 RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
 RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
 RL beta 4 subunits";
 RL J. Mol. Neurosci. 7:217-228(1996).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=97162233; PubMed=9009220;
 RA Groot Kormelink P.J., Luyten W.H.M.L.;
 RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
 RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
 RT expression of seven nAChR subunits in the human neuroblastoma cell
 RL line SH-SY5Y and/or IMR-32";
 RL FEBS Lett. 400:309-314(1997).
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=99118870; PubMed=9921897;
 RA Rempel N., Heyers S., Engels H., Slegers E., Steinlein O.K.;
 RT "The structures of the human neuronal nicotinic acetylcholine receptor
 RT beta2- and alpha3-subunit genes (CHRNA2 and CHRNA3)";
 RL Hum. Genet. 103:645-653(1998).
 RN [6]
 RP SEQUENCE FROM N.A., AND VARIANT LEU-21. INS.
 RX MEDLINE=21342809; PubMed=11450844;
 RA Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.;
 RT "Characterization of the human beta4 nAChR gene and polymorphisms in
 RT CHRNA3 and CHRNA4";
 RL J. Hum. Genet. 46:362-366(2001).
 RN [7]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RP SEQUENCE OF 30-503 FROM N.A.
 RC TISSUE=Brain;
 RA Anand R., Lindstrom J.;
 RL Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases..
 RN [9]
 RP SEQUENCE OF 6-493 FROM N.A.
 RC TISSUE=Epidermal keratinocytes;
 RA Arredondo J., Grando S.A.;
 RT "Cloning cholinergic receptors in human keratinocytes";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE AChR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL AChR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

```

CC CC -!- ALTERNATIVE PRODUCTS:
CC CC Event=Alternative splicing; Named isoforms=2;
CC CC Name=1;
CC CC Name=2;
CC CC IsoId=P32297-1; Sequence=Displayed;
CC CC IsoId=P32297-2; Sequence=VSP_000073;
CC CC Note=NO experimental confirmation available;
CC CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC CC -----
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CC CC -----
CC CC EMBL; M86383; AAC84176.1; -
CC CC EMBL; M37981; AAA59942.1; -
CC CC EMBL; U62432; AAB40110.1; -
CC CC EMBL; Y08418; CAA69695.1; -
CC CC EMBL; AJ007783; CAA07682.1; -
CC CC EMBL; AJ007784; CAA07682.1; JOINED.
CC CC EMBL; AJ007785; CAA07682.1; JOINED.
CC CC EMBL; AJ007786; CAA07682.1; JOINED.
CC CC EMBL; AJ007787; CAA07682.1; JOINED.
CC CC EMBL; BC001642; AAH01642.1; -
CC CC EMBL; BC002996; AAH02996.1; -
CC CC EMBL; BC000513; AAH00513.1; -
CC CC EMBL; AF385584; AAK68110.1; -
CC CC EMBL; X53559; CAA37625.1; -
CC CC PIR; A37040; A37040.
CC CC Genew; HGNC:1957; CHRNA3.
CC CC MIM; 118503; -
CC CC GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. ; TAS.
CC CC GO; GO:004889; F:nicotinic acetylcholine-activated cation-se. ; TAS.
CC CC GO; GO:0005215; F:transporter activity; TAS.
CC CC GO; GO:0001165; P:signal transduction; TAS.
CC CC GO; GO:0006832; P:small molecule transport; TAS.
CC CC InterPro; IPR006029; Neu_channel_memb.
CC CC InterPro; IPR006202; Neu_chan_LBD.
CC CC InterPro; IPR006201; Neu_channel.
CC CC Pfam; PF02931; Neur_chan_LBD; 1.
CC CC Pfam; PF02932; Neur_chan_memb; 1.
CC CC PRINTS; PR00252; NRIONCHANNEL.
CC CC TIGRFAMS; TIGR00860; LIC; 1.
CC CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
CC CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
CC CC Transmembrane; Multigene family; Alternative splicing; Polymorphism.
CC CC SIGNAL 1 29
CC CC CHAIN 30 503
CC CC NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
CC CC ALPHA-3 CHAIN.
CC CC DOMAIN 30 238
CC CC TRANSMEM 239 263
CC CC TRANSMEM 271 289
CC CC TRANSMEM 305 326
CC CC TRANSMEM 327 475
CC CC TRANSMEM 476 495
CC CC DISULFID 157 171
CC CC DISULFID 221 222
CC CC ASSOCIATED WITH RECEPTOR ACTIVATION
CC CC (BY SIMILARITY).
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CC MALAV -> MGSGLP (1n isoform 2).
CC CC /FTID=VSP_000073.
CC CC L -> LL.
CC CC /FTID=VAR_013240.
CC CC VSLPALSP -> ALAAPGAVA (IN REF. 2).
CC CC LSPP -> CRA (IN REF. 1).
CC CC D -> GT (IN REF. 1).
CC CC DD -> TT (IN REF. 1).
CC CC I -> S (IN REF. 1).

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FT CONFLICT 430 430 L -> V (IN REF. 1).
SQ SEQUENCE 503 AA; 57309 MW; 8A9EHC5D71AEC7D6 CRC64;

Query Match 37.5%; Score 989.5; DB 1; Length 503;
Best Local Similarity 38.5%; Pred. No. 9.2e-80;
Matches 200; Conservative 92; Mismatches 166; Indels 61; Gaps 5;

QY 1 MAPMLAALALLPVSQEPHEKRLNALLANNYTLERPVANESEPLEVFRGLTLOQII 60
DB 11 LSPRLLLLSLLPVARASEAEHRLFERLFNEIRPVANVSDPVIHFEVMSQLV 70
QY 61 DVEKKNOLLITNLSLEWYNDYLNWNSYGGVKKDLRITPNKLNKPDVLMYNSADSGFD 120
DB 71 KVDENVQIMETNMLKQIWNKYKPNPSDYGAEMRVPQAQIKWKPDIIVLYNNVAGDFQ 130
QY 121 GTVQTNVVRSGGSCLYVPPGIFKSTCKMDIAFFDDQHCMDKFKGWSYTDGNOLDVLK 180
DB 131 VDDTKALLKYTGVTWIPPAIFKSSCKIDVTYFPDYQNCMKFGWSYDKAKIDLVI 190
QY 181 DEAGGDLSDFITNGEYWLIGMPGKKNITYACCEPYVDVVTFTIMIRRLTYFFNLI 240
DB 191 G-SSMNLKDYWESGEWAILKAPGYKHDIKYNCCCEIYDPDITYSLYIRRLPLFTINLI 249
QY 241 CVLSSNALIGFTLPDSDGKLTGLVTLISLWFLNLVAETLPQVSDAIPLLGYENC 300
DB 250 CLLISFLTVLVFYLPSDCGKVTLCISVLSLVFLVLTITETIPSTSLVPIGLIYLLFT 309
QY 301 MFMVASSVLTVVVLYNHYHRTADITHMPQIKSVFLOLWILRMSPGKKITRKTIMN 360
DB 310 MIFVLSIVITVFLVNVHYRTPTHTMPSVKVTFVFLNLLPRVMPMTRP----- 357
QY 361 TRMRELEKRSKSLIANVLDIDDDPRHGGPPPNSTASTGNL-----GPGCS----- 408
DB 358 -----TSNEGNAQPRPLYGAELSNLNCFSRAESKCGKGYPC 395
QY 409 -----IFRTDFRSFVRPSTMEDVGG--GLGSHRHLHLTLRELQFTARMKK 454
DB 396 QDGMCGYCHRRRIKISFNLSANLRSSESVDVLSLSALSPEIKAEIQSVKYIAENKA 455
QY 455 ADEEAELISDMKFAAMVVDRCFLVFVLTFTIIATVAVLL 493
DB 456 QNEAKEIQDDWKVYAMVIDRFLWVFTVLCILGTAGLFL 494

RESULT 8
ACH3_RAT
ID ACH3_RAT STANDARD; PRT; 499 AA.
AC P04757;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
GN CHRNA3 OR ACRA3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86118671; PubMed=3753746;
RA Boulter J., Evans K., Goldman D.J., Martin G., Treco D.,
RA Heinemann S.F.,
RA Patrick J.;
RA "Isolation of a cDNA clone coding for a possible neural nicotinic
RT acetylcholine receptor alpha-subunit.";
RL Nature 319:368-374(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041184; PubMed=2444984;
RA Boulter J., Connolly J.G., Deneris E.S., Goldman D.J., Heinemann S.F.,
RA Patrick J.;
RT "Functional expression of two neuronal nicotinic acetylcholine
RT receptors from cDNA clones identifies a gene family.";

```

Qy	183	AGGDLDFIYNGEWYLI	MPGKKN	TIYTYACCP	EPYVDVT	FTIMIRRR	TLTYFFNL	IPCV	243	
		: :	: :	: :	: :	: :	: :	: :		
Db	188	SSMNLKDYWESG	WAIITK	APYKHEI	KYNCCEE	IYQDITY	SLYIRRL	PLFTIN	IIICL 247	
		: :	: :	: :	: :	: :	: :	: :		
Qy	243	LISSMALLGTT	LPDSGE	KTLGVT	ILLLSLV	FLNLVAET	LPOVSDA	PLLGCTY	FNCIMF 302	
		: :	: :	: :	: :	: :	: :	: :		
Db	248	LISFLTLVFL	YSPDCG	EVKVTLC	ISVLSLV	FLVLIVET	IPSTSLV	PLIGEY	LLFTMI 307	
		: :	: :	: :	: :	: :	: :	: :		
Qy	303	MVASSVLT	VVVVLYN	YHRTAD	IHEMP	QWIKSV	FLQWLP	WILRMS	RP--GKKITRKT-IMM 359	
		: :	: :	: :	: :	: :	: :	: :		
Db	308	FVTLISIV	TVFLN	VHYRTP	TTHTMP	TWKAV	FLNLLP	RVFMFT	RPTSGEGDTPKTRTFY 367	
		: :	: :	: :	: :	: :	: :	: :		
Qy	360	NTRMRLE	LEKERS	-SKSLL	ANVL	DIIDD	FRHG	PPPP	PNSTASTGNLGPCCSIPR----TDFR 415	
		: :	: :	: :	: :	: :	: :	: :		
Db	368	GAELSN	LNCF	SRAD	SKSC-----	KEGYPC	QD	CGCY-----	CHHRRVVISNFS 410	
		: :	: :	: :	: :	: :	: :	: :		
Qy	416	RSFVRP	STMED	VGG--	GLGSH	RELHL	ILREL	QFIT	ARMKRADEAEELISDWKFAAMVVD 473	
		: :	: :	: :	: :	: :	: :	: :		
Db	411	ANITR	SSSESV	NVAVLS	LSALS	SPKEIA	QSVKY	IAENMK	KAONVAKEIQDDWKVYAMVID 470	
		: :	: :	: :	: :	: :	: :	: :		
Qy	474	RFCLFV	FTLTI	ATVALL	493					
		: :	: :	: :	: :	: :	: :	: :		
Db	471	RIFLW	FILV	ILGTAG	LFL 490					
		: :	: :	: :	: :	: :	: :	: :		

RESULT 9

ACH3_BOVIN

ID	ACH3_BOVIN	STANDARD;	PRT;	495 AA.
AC	Q07263;			
DT	01-OCT-1994 (Rel. 30, Created)			
DT	01-OCT-1994 (Rel. 30, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Neuronal acetylcholine receptor protein, alpha-3 chain precursor.			
GN	CHRNA3.			
OS	Bos taurus (Bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RP	[1]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=92319195; PubMed=1620271;			
RT	Criado M., Alamo L., Navarro A.;			
RT	"Primary structure of an agonist binding subunit of the nicotinic			
RL	acetylcholine receptor from bovine adrenal chromaffin cells.";			
RL	Neurochem. Res. 17:281-287(1992).			
CC	-1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN			
CC	EXTENSIVE CHANGING IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND			
CC	LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA			
CC	MEMBRANE.			
CC	-1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT			
CC	TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.			

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DR	EMBL:	X57032;	CANAM0348.1;	
DR	PIR:	S60589;		
DR	InterPro:	IPR006029;	Neu_channel_memb.	
DR	InterPro:	IPR006202;	Neur_chan_LBD.	
DR	InterPro:	IPR006201;	Neur_channel.	
DR	Pfam:	PF02931;	Neur_chan_LBD; 1	
DR	Pfam:	PF02932;	Neur_chan_memb; 1	
DR	PRINTS:	PR00252;	NRIONCHANNEL.	
DR	TIGRFAMs:	TIGR00860;	LIC; 1	
DR	PROSITE:	PS00236;	NEUROTR_ION_CHANNEL; 1	

KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 FW Transmembrane; Multigene family.
 FT SIGNAL 1 21
 FT CHAIN 22 495
 FT
 FT DOMAIN 22 230
 FT TRANSMEM 231 255
 FT TRANSMEM 263 281
 FT TRANSMEM 296 318
 FT TRANSMEM 319 467
 FT TRANSMEM 468 483
 FT DISULFID 149 163
 FT DISULFID 213 214
 FT
 FT CARBOHYD 45 45
 FT CARBOHYD 162 162
 FT SEQUENCE 495 AA; 56914 MW; 322825629821EA07 CRC64;
 Query Match 36.88; Score 970.5; DB 1; Length 495;
 Best Local Similarity 39.88; Pred. No. 4.3e-78;
 Matches 198; Conservative 93; Mismatches 181; Indels 25; Gaps 7;
 QY 5 LAALALLLPVSEQGPHERKLLNALLANTLERPVANESEPLEVRFGTLTLOQIIDVDE 64
 DB 7 LRRLLLLLLPVASTDAERHLERLFEDYNEIRPVANVSDPVIIQFVMSQLVKVDE 66
 QY 65 KNOLLITNIWLSLENDYNIWRNDSYGGVKDLRITPNKLUKPDVLMYNSADSGFGDTYQ 124
 DB 67 VNOIMETNLKQIWNIDYKLNWPSDYDGAEFMRVPAEKIWKPDIVLYNNAVGDFQVDDK 126
 QY 125 TNVVRSGGCLYVPGIFKSTCKMDIAWPFDDOCHDKMFGSWYDGNOLDLVLKDEAG 184
 DB 127 TKALLKYTGVTWIPPAIFKSSKIDVTFYFQYQNTKMFQGSWSDYKAKIDLVLIG-SS 185
 QY 185 GDLSDFTNGEWLIGMPGKNITTYACCPPEPVVDVFTIMIRRTLYFFNLIVPCVLI 244
 DB 186 MNLKDYWESGEWAIKAPGVKHKDKYCNCEIYDITYSLYIRRLFYINLIPLCLI 245
 QY 245 SSMAILGFTLPDPSGEKLTGVTLLSLTVFLNLVAETLPQVSDAIPLLTYNCINFMV 304
 DB 246 SFTLVFLYLPDSCGERVTCISVLLSLTVFLVITETIPSTSLVPLIGEYLLFTMIFV 305
 QY 305 ASSVVLNVVNLVHRTADITHMPWIKSVFLQWLPILWLRMSPGK---KITRKTIMMNT 361
 DB 306 TSLVITVFLNVHRYTPHTTHPAWVKWITFLNLLPRVMTFRPASNEGTFQRPYSA 365
 QY 362 RMRELELKRSSKSLANVLDDDFDRHGGPPPNSTASTGNLPGCSIFR---TDFRRSF 418
 DB 366 ELSNLNCFSLIESKVC-----KEGYP-----CODGLCG-YCHHRRAKISNFSANL 409
 QY 419 VRPSTMEDVGG--GLGSHHRELHLILRELQFITARMKKADEEAEELISDWKFAAMVDVDFC 476
 DB 410 TRSSSSSEDAVLSLSALSPEIKAEIQSVKYIAENMKQAQNEAKEIQDDWKYVAMVIDRIF 469
 QY 477 LFVETLTIATVAVLL 493
 DB 470 LWVFLYLCILGTAGLFL 486

RESULT 10

ACHI_DROME
 ID ACHI_DROME STANDARD; PRT; 567 AA.
 AC P09478; Q9VC74;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Acetylcholine receptor protein, alpha-like chain 1 precursor.
 GN NACK-ALPHA-96AA OR ACRB OR ALS OR ACR96AA OR C65610.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;

RN SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=88283626; PubMed=2840281;
 RA Bossy B., Ballivet M., Spierer P.;
 RT "Conservation of neural nicotinic acetylcholine receptors from
 RL Drosophila to vertebrate central nervous systems.";
 RMBO J. 7:611-618(1988).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heilmann T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei X., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Stapleton M., Strong R.,
 RA Spier E.R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodard T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 [3]
 RN REVISIONS.
 RP STRAIN=Berkley;
 RC MEDLINE=22426069; PubMed=12537572;
 RX Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 RL systematic review";
 RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: CNS IN EMBRYOS.
 CC -!- DEVELOPMENTAL STAGE: LATE EMBRYONIC, LATE PUPAL AND SECOND INSTAR
 CC LARVAE STAGES.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

Db 203 SVENDILEVPAVRNEKFTCCDPYLDITFNITMRRKTLFTYVNLIIIPCMGISFLVLFV 262

Qy 253 TLPPDSGEKLTGVTILLSTVFLNLVAETLPQVSDAIPLLIGTYFNCIMFMWASSVLT 312

Db 263 YLPSDSGEKVSLSILLSTVFLLLAEIIPPTSLVVLGKFLVFTMLDFTSICVT 322

Qy 313 VVLYNHRTADIHEMPOWIKSVFLQWLPWILNRSRGCKI---TRKTIMMTRMRELELK 369

Db 323 VVLYNHFRSPQTHMTSPWRRVFIHVLPRLLVRRRPHYRLDPRHSFAGLVGTAGETTLW 382

Qy 370 ERSGKSLANVLDDDDFRHGPNNSTASTGNLGP--GCSIFRTDFRRSFVRPSTMEDV 427

Db 383 DESPGV-----PAPRPPPCAPPLAPCAACA-----PAPAL 416

Qy 428 GGGIGSHRR--ELHLRLRELQFTIARMKKADEAELISDMKFAAMVVVDRCLFVFTFTI 485

Db 417 CDALRRWHRCPELHKADGINIYADOTRKEESTRVKEDWKYVAVMLDRFLFIETLAVV 476

Qy 486 IATVAVLLSAP 496

Db 477 VGSAGIILQAP 487

RESULT 13

ACH1_SCHGR

ID ACH1_SCHGR STANDARD; PRT; 557 AA.

AC P23414;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Acetylcholine receptor protein, alpha-L1 chain precursor.

OS Schistocerca gregaria (Desert locust).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.

OX NCBI_TaxID=7010;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=91092263; PubMed=1702381;

RA Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,

RA Darlison M.G., Sattelle D.B., Barnard E.A.;

RT "Sequence and functional expression of a single alpha subunit of an

RT insect nicotinic acetylcholine receptor."

RL EMBL J. 9:4391-4398(1990).

CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN

CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND

CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA

CC MEMBRANE.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

CC -----

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CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or

CC send an email to license@isb-sib.ch).

CC -----

DR EMBL: X55439; CAA35081.1; -

DR PIR: S12359; S12359.

DR InterPro: IPR006029; Neu_channel_memb.

DR InterPro: IPR006202; Neu_chan_LBD.

DR InterPro: IPR006201; Neu_channel.

DR Pfam: PF02931; Neu_chan_LBD; 1

DR Pfam: PF02932; Neu_chan_memb; 1

DR PRINTS: PR00252; NRIONCHANNEL.

DR TIGRFS: TIGR00860; LIC; 1.

DR PROSITE: PS00236; NEUROTR ION CHANNEL; 1.

KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;

KW Transmembrane; Multigene family.

FT SIGNAL 1 23 POTENTIAL.

FT SIGNAL 24 557 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1

FT DOMAIN 24 244

FT TRANSMEM 245 266

FT TRANSMEM 274 294

FT TRANSMEM 308 329

FT DOMAIN 330 500

FT TRANSMEM 501 523

FT DISULFID 151 165

FT DISULFID 224 225

FT CARBOHYD 47 47

FT CARBOHYD 235 235

FT DOMAIN 382 400

FT DOMAIN 406 422

SQ SEQUENCE 557 AA; 63026 MW; 168389C887DFE3E CRC64;

Query Match 35.8%; Score 944; DB 1; Length 557;

Best Local Similarity 36.9%; Pred. No. 1.1e-75;

Matches 201; Conservative 96; Mismatches 181; Indels 66; Gaps 7;

Qy 1 MAPMLAALALLLPVSEQGPEKRLNALLANYNLTLPVANESEPLEVRFGLTQQII 60

Db 5 LPPMLLLLLLLLHPAAANPDARKLYDOLLSNYNRLRPVSNNDTVLVKGRLSLQI 64

Qy 61 DVDEKNOLLITNLSLEWYNDYLNWNSYGGVKDLRITPNKLPDVLNYSADGFD 120

Db 65 DLNKKQILTTNVWLEHEMWDHFRWDPAEYGGVTELYVSEHILWLPDIYLYNNAEYV 124

Qy 121 GTYTNNVVRSGSCLYVPGIPIKSTCKMDIANFPDDOHCMDKFGSWTVDGNOLDV-- 178

Db 125 VTTMTKAVLHHTGKVVVMTTPAIFKSCIEDVRYFPDQOTCFMKFGSWTVDGQIDLKHI 184

Qy 179 -----LKDEAGDGLSDFITNGEWYLGMPKKNITTYACCPPEYVDVTFIMIRRTLY 232

Db 185 NQYDDNKVKVGDILREYVPSVEMDILGVPAERHEKYPCCAEYPDIFENILRRKTLF 244

Qy 233 YFENLIVPCVLISSMALLGTLPPDGEKLTGVTILLSTVFLNLVAETLPQVSDAIP 292

Db 245 YTVNLIVPCVGISYLSVLVFLPADSGEKIALCISILLSTQTFMFLIETIPSTSLAPL 304

Qy 293 LGTYNFCIMFMWASSVLTVVVLYNHRTADIHEMPOWIKSVFLQWLPWILNRSRGCK-- 350

Db 305 LGKYLFTVVLGSLVVTITVNLVNHVKPSTHMAPWVRKVFIIRLKLMLMRVPEQLL 364

Qy 351 -KITRKTIMMTRMRELEKERSKSLA--NYLIDIDDDFRH----- 389

Db 365 ADLASKRLRLRHAKNSLSAAAAAASAAASPSLSRHHHLHQHQLHLHLQ 424

Qy 390 GPPPPNST-ASTGNLPGGCSIFRTDFRRSFVRPSTMEDVGGGLGS----- 433

Db 425 RPGGCGNLHSATNRFSGSAGAF-----GGLPSVVGDLGSLSDVATRK 466

Qy 434 -HREHLHLILRELQFTIARMKKADEAELISDMKFAAMVVVDRCLFVFTFTIATVAVL 492

Db 467 KYFELEKAIHNVLFIONHMQRDEDAEDQDQMGFVAVMLDRFLFIETIASIVGTAIL 526

Qy 493 LSAP 496

Db 527 CEAP 530

RESULT 14

ACH2_DROME

ID ACH2_DROME STANDARD; PRT; 576 AA.

AC P17644; Q9VC73;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Acetylcholine receptor protein, alpha-like chain 2 precursor.

GN NACR-ALPHA-96AB OR ACR9 OR SAD OR ACR96AB OR CG6844.

OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Db	94	KLKRDWMEYDGETFLRPADKIRWPDVLYNNAGVDFQVEGTRKALLXNGMTWTPPAI	153
QY	143	FKSTCKMDIAWFPDDQHQCDMKGWTYDGNQLDLVLKDEAGG--DLSDFTINGEWYLI	200
Db	154	FKSCSPMDITFFPDHONCSLKFGSWTYDKAEIDLLI---IGSKVMDMDFWENSEWEI	210
QY	201	MPGKNNTITYACCPPEYVDVTFTIMRRRTLYFFNLIVPCVLISSMALLGFTLPDPSGE	260
Db	211	ASGYKHDIKYNCCBEEIYDTISFYIRRLPMFYTINLIICLFI SFLVLYFLPSDCGE	270
QY	261	KLTGVTILLSLTVFLNLVAETIPOVSDAIPLLGTYFCIMFMWASSVVLTVVVLNYHHR	320
Db	271	KVTLICISVLLSLTVFLIVITETIPSTSLVVPLVGEYLLFTMTI FVTLISVTVTVFLNIHYR	330
QY	321	TADITHEMPWIKSVFLQWLWILMRSPGCKITRKTIMMTRMRELELEKRSKSLIANV	380
Db	331	TPTTHTPRWVTVTKVFLKLLPOVILLRMPDLK-TRGT---GSDAVPRGLARRPAKGLAS-	385
QY	381	LDIDDDFRHGPP-----PPNSTASTGNLPGCSIFTRDFRRSFVRPS--TMEVVG	428
Db	386	-----HGEPRHLKCFCHKSNELA-----TSKRRLSHOPLQWVVEN--	422
QY	429	GGLGSHHRELHLILQFOTARMKADAEAEALISDWKFAAMVDFCLFVFTFTIITAT	488
Db	423	---SEHSPVEDVINSVOFI AENKSNHETKEVEDDKVKYAMVVDVFLWFIILVCVFEGT	479
QY	489	VAVLL 493	
Db	480	AGLEF 484	

Search completed: August 13, 2003, 15:26:13
Job time : 12.4907 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:45 ; Search time 18.7131 Seconds
(without alignments)
2574.698 Million cell updates/sec

Title: US-09-303-232-6
Perfect score: 2640
Sequence: 1 MAPMLALALLLPVSEQG.....LFTTIATVAVLLSAPHIIVQ 501
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1260	47.7	502	1 ACHUA7	nicotinic acetylch
2	1255.5	47.6	502	2 A57175	nicotinic acetylch
3	1253	47.5	502	2 JN0113	nicotinic acetylch
4	1252.5	47.4	502	2 G02259	alpha 7 neuronal n
5	1246.5	47.2	502	2 T01378	nicotinic receptor
6	1237.5	46.9	498	2 S68588	nicotinic acetylch
7	1226.5	46.5	511	2 JH0173	alpha-bungarotoxin
8	1132	42.9	461	2 T25671	hypothetical prote
9	1083.5	41.0	542	2 T19862	hypothetical prote
10	1081	40.9	560	2 T19622	hypothetical prote
11	989	37.5	503	2 A53956	nicotinic acetylch
12	982.5	37.2	502	2 A37040	nicotinic acetylch
13	970.5	36.8	495	2 S60589	acetylcholine rece
14	970.5	36.8	499	2 A24572	nicotinic acetylch
15	964.5	36.5	567	1 ACPFA1	nicotinic acetylch
16	944	35.8	557	2 S12359	nicotinic acetylch
17	943	35.7	576	1 ACPFA2	nicotinic acetylch
18	929.5	35.2	494	2 T09289	nicotinic acetylch
19	924.5	35.0	528	1 ACPH2N	nicotinic acetylch
20	919.5	34.8	512	2 A37014	nicotinic acetylch
21	919	34.8	511	2 A40110	nicotinic acetylch
22	910	34.5	500	2 S12899	nicotinic acetylch
23	909.5	34.5	495	2 B35721	nicotinic acetylch
24	906.5	34.3	517	2 A30992	probable nicotinic
25	906	34.3	457	1 ACBOA1	nicotinic acetylch
26	905	34.3	457	1 ACHUA1	nicotinic acetylch
27	901	34.1	521	1 ACPFNN	nicotinic acetylch
28	900	34.1	503	2 JH0174	nicotinic acetylch
29	897.5	34.0	627	2 JC4021	nicotinic acetylch

ALIGNMENTS

RESULT 1

ACHUA7

Nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 31-Jan-1997 #text_change 22-Jun-1999
C:Accession: I37185; A54194; S60309
R:Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.
Mol. Pharmacol. 45, 546-554, 1994
A:Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from th
omers expressed in Xenopus oocytes.
A:Reference number: I37185; MUID:94195283; PMID:8145738
A:Accession: I37185
A:Status: translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-502 <P>EN>

A:Cross-references: EMBL:X70297; NID:9496606; PION:CAA9778.1; PID:9496607

A:Experimental source: brain neuroblastoma cell line SHSY-5Y

R:Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S.

Genomics 19, 379-381, 1994

A:Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotini
A:Reference number: A54194; MUID:94245214; PMID:8188270
A:Accession: A54194

A:Molecule type: mRNA

A:Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <CHI>

A:Cross-references: GB:223141; NID:9457736; PIDN:CAA80672.1; PID:9457737

A:Experimental source: retina

C:Comment: this acetylcholine receptor is blocked by alpha-bungarotoxin and is locali
C:Genetics:
A:Gene: GDB:CHRNA7
A:Cross-references: GDB:138751; OMIM:118511
A:Map position: 15q14-15q14

A:Note: defects in this gene have been associated with mental retardation and schizop

C:Complex: the functional receptor molecule is a heteropentamer with two alpha chains

C:Superfamily: acetylcholine receptor

F:1-23/Domain: signal sequence #status predicted <SIG>

F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr

F:231-254/Domain: transmembrane #status predicted <TP1>

F:262-280/Domain: transmembrane #status predicted <TR2>

F:296-317/Domain: transmembrane #status predicted <TR3>

F:470-488/Domain: transmembrane #status predicted <TR4>

F:46-90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:150-164/Disulfide bonds: carbonyl (Ser) (covalent) #status predicted

F:365,413/Binding site: phosphate (Thr) (covalent) #status predicted

F:445/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 47.7%; Score 1260; DB 1; Length 502;

Best Local Similarity 48.5%; Pred. No. 2 6e-99;

Matches 247; Conservative 75; Mismatches 137; Indels 50; Gaps 6;

Qy 12 ALLPVSDGQPHKRLNALLANTLERPVANSEPLEVFGUQLQOIIDVSKNOLLIT 71
 Db 15 SLLHVSQGFQKLYKELYNKPLNPLRPVANDSQPLTVYFSLQLQIMDVDEKNQVLT 74
 Qy 72 NIWLSLEWNYNLRWSDYGVKDLRITPNKLNKPDVLMYNSADGFGDTYOTNVVRS 131
 Db 75 NIWLSWTDHYLQWNVSEYPGVKTVPDQGIWKPDILLYNSADERDFATHTNVLVS 134
 Qy 132 GGSCLYVPPGIFKSTCKMDIAWPFDDQCHDMKFGSWTYDGNOLDLVKDEAGDLSDFI 191
 Db 135 SGHCQYLPPIKSSCYIDVRWPFDDQCHDMKFGSWTYDGNOLDLVKDEAGDLSDFI 191
 Qy 192 TNGEWYLGMPGKNTITYACCPPEYVDVFTTIRRRRTLYFFNLLVPCVLISMAJG 251
 Db 192 PNGEDLVGIPGRKSERFEYCKPEYPDVFTVMTMRRRTLYGLNLLIPCVLISALALLV 251
 Qy 252 FTLPDPSGEKLTGLVITLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFYASSVLT 311
 Db 252 FLTPADSGEKISGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIYGLSVVVT 311
 Qy 312 VVVLNYHRTADIEHMPQWIKSVFLQWLPWILRMSRPGKKTIRKTIIMNTRMRELELKER 371
 Db 312 VIVLOYHHDPDGGKMPKTRVILLNWCANFLRMKRPGEKVPACQHKORCSLASVEM 371
 Qy 372 SSKSLANVLIDDDFRHGGPPPNSTASTGNL-----GPGCSIFRT 412
 Db 372 SAV-----GPPP-----ASGNLLYIGRGLDGVHCVPDTPDSGVVCG---- 408
 Qy 413 DFRSFVPRSTMEDV---GGGLGSHHRELHLILRELOFITARMKKADEAEELISDWKFAAM 470
 Db 409 ---RMACSPHDEHLLGGOPGPDPLAKILEVRYIANFRQDESEAVCEWKFAC 465
 Qy 471 VDRFCLFVFTLTIIATVALLSAPHII 499
 Db 466 VDRCLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 2
 A57175
 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
 C:Accession: A57175
 R:Orr-Urtreger, A.; Seldin, M.F.; Baldini, A.; Beaudet, A.L.
 Genomics 26, 399-402, 1995
 A:Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine receptor
 A:Reference number: A57175; MUID:95324936; PMID:7601470
 A:Accession: A57175
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-502 <ORR>
 A:Cross-references: GB:L37663; NID:g790853; PIDN:AAC42053.1; PID:g790854
 A:Superfamily: acetylcholine receptor
 C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;
 F:1-23/Domain: signal sequence #status predicted <Sig>
 F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain; neuronal #status predicted
 F:21-254/Domain: transmembrane #status predicted <TR1>
 F:262-280/Domain: transmembrane #status predicted <TR2>
 F:296-317/Domain: transmembrane #status predicted <TR3>
 F:470-488/Domain: transmembrane #status predicted <TR4>
 F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted
 F:415/Binding site: phosphate (Thr) (covalent) #status predicted
 F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 47.68; Score 1255.5; DB 2; Length 502;
 Best Local Similarity 49.68; Pred. No. 6.3e-99;
 Matches 249; Conservative 78; Mismatches 148; Indels 27; Gaps 7;

Qy 8 LALLPVSEQPHKRLNALLANTLERPVANSEPLEVFGUQLQOIIDVDEKN 66
 Db 10 LALAAALLVSLQGEFORRLKELVKNPLNPLRPVANDSQPLTVYFSLQLQIMDVDEKN 69

Qy 67 QLLITNIWLSLEWNYNLRWSDYGVKDLRITPNKLNKPDVLMYNSADGFGDTYOTN 126
 Db 70 QVLTITNIWLSWTDHYLQWNVSEYPGVKNVREPDQGIWKPDILLYNSADERDFATHTN 129
 Qy 127 VVVRSGSCLYVPPGIFKSTCKMDIAWPFDDQCHDMKFGSWTYDGNOLDLVKDEAGD 186
 Db 130 VLVNASHGHCQYLPPIKSSCYIDVRWPFDDQCHDMKFGSWTYDGNOLDLVKDEAGD 186
 Qy 187 LSDFITNGEWYLGMPGKNTITYACCPPEYVDVFTTIRRRRTLYFFNLLVPCVLIS 246
 Db 187 ISSYIPNGEWDLGIPGRKSERFEYCKPEYPDVFTVMTMRRRTLYGLNLLIPCVLISA 246
 Qy 247 MALLGFTLPDPSGEKLTGLVITLLSLTVFLNLVAETLPQVSDAIPLLGTYFNCIMFYAS 306
 Db 247 LALLVLLPADSGEKISGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIYGL 306
 Qy 307 SVVLTVVVLNYHRTADIEHMPQWIKSVFLQWLPWILRMSRPGKKTIRKTIIMNTRMREL 366
 Db 307 SVVVTIVLRYHHDDPDGGKMPKTRVILLNWCANFLRMKRPGEKVPACQHKORCSL 366
 Qy 367 ELKERSS---KSLANVLIDDDFR-----HGPPPNSTASTGNLPGCSIFRTDFRRS 417
 Db 367 ASVELSAGAGPPTSNGNLLYI---GFRGLEGMHCAPTDPDGVWCGR---ACSPHDEHLMH 422
 Qy 418 FVPRSTMEDVGGGLGSHHRELHLILRELOFITARMKKADEAEELISDWKFAAMVDRFCL 477
 Db 423 GTHPSDGP-----DLAKILEVRYIANFRQDESEVICSEMKFAACVDRCL 472
 Qy 478 FVFTLTIIATVALLSAPHII 499
 Db 473 MAFSVFTICTIGILMSAPNFV 494

RESULT 3
 JN0113
 nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
 N:Alternate names: alpha-bungarotoxin-binding protein alpha chain
 C:Species: Gallus gallus (chicken)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
 C:Accession: JN0113; JH0172; S28018; B25738; S26566
 R:Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.
 Neuron 5, 847-856, 1990
 A:Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is development
 A:Reference number: JN0113; MUID:91097796; PMID:1702646
 A:Accession: JN0113
 A:Molecule type: DNA
 A:Residues: 1-502 <COU>
 A:Cross-references: GB:X68586; NID:g287756; PIDN:CAA48576.1; PID:g287757
 A:Experimental source: white leghorn; brain
 R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
 Neuron 5, 35-48, 1990
 A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MABs reveal subtypes of t
 A:Reference number: JH0172; MUID:90315158; PMID:2369519
 A:Accession: JH0172
 A:Molecule type: mRNA
 A:Residues: 1-502 <SCH>
 A:Cross-references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078
 A:Experimental source: brain
 R:Matter-Sadzinski, L.; Hernandez, M.C.; Rostocil, T.; Ballivet, M.; Matter, J.M.
 EMBO J. 11, 4529-4538, 1992
 A:Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter
 A:Reference number: S28018; MUID:93049204; PMID:1425587
 A:Accession: S28018
 A:Molecule type: DNA
 A:Residues: 1-18 <MAS>
 A:Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320
 A:Experimental source: white leghorn; erythrocyte
 R:Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.;
 Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
 A:Title: Brain and muscle nicotinic acetylcholine receptors are different but homolog
 A:Reference number: A94055; MUID:85270494; PMID:3860855
 A:Accession: B25738
 A:Molecule type: protein

A:Residues: 24-25, 'ET', 28-41, 'X', 43-45, 'X', 47 <CON>
C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized
C:Genetics:
A:Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
C:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein;
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-302/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted
F:231-254/Domain: transmembrane #status predicted <TR1>
F:262-280/Domain: transmembrane #status predicted <TR2>
F:296-317/Domain: transmembrane #status predicted <TR3>
F:470-488/Domain: transmembrane #status predicted <TR4>
F:46,90,133/Binding site: carboxylate (Asn) (covalent) #status predicted
F:365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #status predicted
F:415/Binding site: phosphate (Thr) (covalent) #status predicted
F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 47.5%; Score 1253; DB 2; Length 502;
Best Local Similarity 48.8%; Pred. No. 1e-98;
Matches 250; Conservative 81; Mismatches 145; Indels 36; Gaps 8;

QY 2 APMALALLALLPVSEQPEHKEKRLNALLANYTLERPVANSEPLEVRFGTLTQOIID 61
DB 5 ALMLWLLAAGLVRESLQGEFQKLYKELLYNPLERPVANDSPLTYFTLSLQIMD 64

QY 62 VDEKNQLLITNWLSEWNYDLRWNDSEYGGVKDLRITPNKLMKPDVLMYNSADEGPDG 121
DB 65 VDEKNQVLTNWLQWMTDHYLQWNVSEYPGVKVRFDPDGLIMKPDILLYNSADERFPA 124

QY 122 TYQTNVVRSGSCLYVPPGIFKSTCKMDIAWFPDDQDHCMDKFGSWTYDGNLDLVLKD 181
DB 125 TPTNTNVLVNSGHCQYLPFGKRSFYECCKEPYDVTFTVTRRRRTLYGLNLLIPC 184

QY 182 EAGGDLSDITNGEWYLGMPGKNTITYACCPYVDVTFITMIRRTLYYFFNLIVPC 241
DB 185 ---ADISGYISNGEWDLVGIPKRTSEFYECCKEPYDVTFTVTRRRRTLYGLNLLIPC 241

QY 242 VLISSMALGFTLPDPSGKELGLVITLLSVFLNVAETLPQVSDAIPLLGTGFNCIM 301
DB 242 VLISALALLVFLPADSGEKISLIGITVLLSVFLLVAEIMPATSDSVPLIAQYFASTM 301

QY 302 FVASSVLTIVVLYNHHRTADIEHPQWIKSVFLOLWPLIRMSRPGKIKTRKTMNT 361
DB 302 IIVGVSVTVIVLQYHHDDPGGKMPKWTIRVILLNWCAMFLMRKPGEDKVRPACQHKQ 361

QY 362 RMRELKRSKSKS-----LLANVLIDDDFR-----HGPPPNSTASTNGLPGGCSIFRT 412
DB 362 RCCLSSMEMNTVSGOCSNGNMLYI--GFRGLDGVHCTPTDWSGVICGM--TCS---- 413

QY 413 DFRSRVPRSTWEDVGGGLGSHH-----RELHLILRELQFITARMKKADEEAELISDKWF 467
DB 414 -----PTEENL---LHSGHPSEGDPLAKILEEVRYIANRFRCDSEAVCSEW 462

QY 468 AAMVDRCLFVFTFTIATVAVLLSAPHII 499
DB 463 AASVDRCLMAFSVFTIICITIGLMSAPNFV 494

RESULT 4
G02259
alpha 7 neuronal nicotinic acetylcholine receptor - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C:Accession: G02259
R:Leonard, S.
submitted to the EMBL Data Library, November 1995
A:Reference number: H00936
A:Accession: G02259
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <LEO>
A:Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077
C:Superfamily: acetylcholine receptor

Query Match 47.4%; Score 1252.5; DB 2; Length 502;
Best Local Similarity 48.4%; Pred. No. 1.1e-98;
Matches 249; Conservative 74; Mismatches 140; Indels 51; Gaps 7;

QY 8 LALLA--LLPVSQGPHEKRLNALLANYTLERPVANSEPLEVRFGTLTQOIIDVDEKN 66
DB 10 LALAAALLHVSQGEFQKLYKELLYNPLERPVANDSPLTYFTLSLQIMDVEKN 69

QY 67 QLLITNWLSEWNYDLRWNDSEYGGVKDLRITPNKLMKPDVLMYNSADEGPDGYQTN 126
DB 70 QVLTNINLQWMTDHYLQWNVSEYPGVKVRFDPDGLIMKPDILLYNSADERDATFTN 129

QY 127 VVVRSGSCLYVPPGIFKSTCKMDIAWFPDDQDHCMDKFGSWTYDGNLDLVLKDEAGD 186
DB 130 VLVNPSGHCQYLPFGGIFKSSCYIDVRWFPDVQGHCKLFGSGWYDGLQMOE---AD 186

QY 187 LSDFTNGEWYLGMPGKNTITYACCPYVDVTFITMIRRTLYYFFNLIVPCVLIS 246
DB 187 ISGYIPNGEWDLVGIPKRSERYECCKEPYDVTFTVTRRRRTLYGLNLLIPCVLISA 246

QY 247 MALLGFTLPDPSGKELGLVITLLSVFLNVAETLPQVSDAIPLLGTGFNCIMFVAS 306
DB 247 LALLVFLPADSGEKISLIGITVLLSVFLLVAEIMPATSDSVPLIAQYFASTMIIVGL 306

QY 307 SVVLTIVVLYNHHRTADIEHPQWIKSVFLOLWPLIRMSRPGKIKTRKTMNTRMREL 366
DB 307 SVVTVTVLQYHHDDPGGKMPKWTIRVILLNWCAMFLMRKPGEDKVRPACQHKQRCSL 366

QY 367 ELKERSKSKLLANVLIDDDFRHGPPPNSTASTGNL-----GPGC 407
DB 367 ASVMSAVA-----PPP-----ASGNLLYIGFRGLDGVHCTPTDPSGVVC 407

QY 408 SIFRTDFRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEEAELISDW 465
DB 408 G-----RMACSPHDEHLLHGQPGGPDOLAKILEEVRYIANRFRCDSEAVCSEW 460

QY 466 KFAAMVDRCLFVFTFTIATVAVLLSAPHII 499
DB 461 KFAACVVDRLCLMAFSVFTIICITIGLMSAPNFV 494

RESULT 5
T01378
nicotinic receptor alpha 7 chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C:Accession: T01378
R:Sequeira, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W.
J. Neurosci. 13, 596-604, 1993
A:Title: Molecular cloning, functional properties, and distribution of rat brain alpha
A:Reference number: Z14310; MUID:93147931; PMID:7678857
A:Accession: T01378
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <SEG>
A:Cross-references: EMBL:S53987; NID:g264770; PIDN:AA25224.2; PID:g5705903
A:Experimental source: brain
C:Superfamily: acetylcholine receptor

Query Match 47.2%; Score 1246.5; DB 2; Length 502;
Best Local Similarity 49.4%; Pred. No. 3.7e-98;
Matches 248; Conservative 78; Mismatches 149; Indels 27; Gaps 7;

QY 8 LAL--LALLPVSEQGPHEKRLNALLANYTLERPVANSEPLEVRFGTLTQOIIDVDEKN 66
DB 10 LALAAALLHVSQGEFQKLYKELLYNPLERPVANDSPLTYFTLSLQIMDVEKN 69

QY 67 QLLITNWLSEWNYDLRWNDSEYGGVKDLRITPNKLMKPDVLMYNSADEGPDGYQTN 126
DB 70 QVLTNINLQWMTDHYLQWNVSEYPGVKVRFDPDGLIMKPDILLYNSADERDATFTN 129

QY 127 VVVRSGSCLYVPPGIFKSTCKMDIAWFPDDQDHCMDKFGSWTYDGNLDLVLKDEAGD 186

Db 130 VLVNASHCOYLPPGIFKSSCYIDVRWFFPDVQCKLKFGWSYGGWSLDLQOE---AD 186
 Qy 187 LSFDFITNGEWYLGMPGKKNITACCPYVVDVTFIMIRRTLYFFNLVPCVLISS 246
 Db 187 ISSVIPNGEWDLMGIPGKRNEKFEYCKEYPPDVTVTVTRRTLYGLNLLIPCVLISA 246
 Qy 247 MALLGFTLPDPSGEKLTGLVTLLSLTVFLNVAETLPQVSDAIPLLGTTFNCFMFWAS 306
 Db 247 LALLVFLPADSGEKISIGITVLISLTVFVLLVAEIMPATSDSVPLTAQYFASTMTIIVGL 306
 Qy 307 SVLTVVVLVNYHRTADIEHMPQWIKSVFELQWLPWILRMSRPGKKTIRKTMIMNTRMREL 366
 Db 307 SVVTVIVLRYHHDDPGGRKPKWTRILLNWCANFLMRKPGEDKVRPAQCHKPRCSL 366
 Qy 367 ELKERSS---KSLANVLIDDDFR-----HGPPPPNSTASTGNLGGGSIERTDFRRS 417
 Db 367 ASVELSAGAGPPTSNGNLLYI--GFRGLEGMHCAPTDSGVVCGRL--ACSPTHDEHLHM 422
 Qy 418 FVRPSTMEDVGGGLGSHHRELHLILRELQFIATMKKADEAEELISDKWFAAMVVDVRFCL 477
 Db 423 GAHPSDGDP-----DLAKILEVRVIANRRCODESEVICSEWKFACVVDPLCL 472
 Qy 478 FVFTLFTIATVALLSAPHII 499
 Db 473 MAFSVFTIICITIGILMSAPNFV 494

RESULT 6
 S68588
 nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabditis e
 C:Species: Caenorhabditis elegans
 C:Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999
 C:Accession: S68588; S57496
 R:Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.
 J. Mol. Biol. 258, 261-269, 1996
 A:Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.
 A:Reference number: S68587; MUID:96196478; PMID:8627624
 A:Accession: S68588
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-498 <BAL>
 A:Cross-references: EMBL:X83887; NID:g872087; PIDN:CAA58764.1; PID:g872088
 C:Superfamily: acetylcholine receptor
 C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <MAT>

Query Match 46.9%; Score 1237.5; DB 2; Length 498;
 Best Local Similarity 47.5%; Pred. No. 2.1e-97;
 Matches 245; Conservative 80; Mismatches 140; Indels 51; Gaps 9;
 Qy 2 APLAALALLPVSQGPHEKRLNALLANYNTLPRVANESPELEVRFGTLQIID 61
 Db 15 APTGLSL-----QERLYEDLMRYNRLRPNVANHSEPTVHLKVALQIID 61
 Qy 62 VDERKQLITNIMLSLEWNYNLRWNSDEYGGVKDLRITPNKLNKPKDVLNYSADGFDG 121
 Db 62 VDERKQVYVNAWLDYTWNDYLNVDKAEYGNITDVRFPAGKINPKDVLNYSVDTFNDS 121
 Qy 122 TYQTNVVRSGGCLYPPGIFKSTCKMDIAWFFDDQCHDMKFGSWTYDGNOLDVLKD 181
 Db 122 TYQTNMIVYGLVHHVWPPGIFKISCKIDIQWFFDEQCKFFKFGSWTYDGYKLD--LQP 179
 Qy 182 EAGG-DLSDFITNGEWYLGMPGKKNITACCPYVVDVTFIMIRRTLYFFNLVPCVL 240
 Db 180 ATGGFDISEYLSNGEAWPLTTVERNEKFYCCPEYPDVHFVHLHMRRTLYYGFNLMP 239
 Qy 241 CVLISSMALLGFTLPDPSGEKLTGLVTLLSLTVFLNVAETLPQVSDAIPLLGTTFNCF 300
 Db 240 CILTTLMTLLGFTLPDPAAGEKITLIQITVLLSICFFLSIVSEMSPTSEAVPLLGIFTC 299
 Qy 301 MFWASSVVLVNYHRTADIEHMPQWIKSVFELQWLPWILRMSRPGKKTIRKTI--M 358

Db 300 MIVVSTAEVTVVNLNHYETPTHDMGPWTRNLLLYWIPILRMKRGHNLVASPLS 359
 Qy 359 MNTRMRELELKERSSKSLANVLID-----IDDFRHGPPPPNSTASTGNLGPCCS 408
 Db 360 FSTK-----PNRHSSELIIRNIKDNEHLSRANSFADACRLNQYIMTQSYVSNGLTSLG-S 412
 Qy 409 IFRDTRFRSFRVSTMEDVGGGLGSHHRE-----LHLILRELQFIATMKKADEAEELIS 463
 Db 413 I-----PSTMISSNGTTDVSQATLILHRIYHELKIVTARMIEGDKREQACN 461
 Qy 464 DKWFAAMVDRFCFLVFETFTIATVALLSAPHII 499
 Db 462 NWKFAAMVDRCLCYVETIIVSTIGIFWSAPLV 497

RESULT 7
 JH0173
 alpha-bungarotoxin-binding protein alpha-2 chain precursor - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999
 C:Accession: JH0173
 R:Schoeffer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
 Neuron 5, 35-48, 1990
 A:Title: Brain alpha-bungarotoxin binding protein cDNAs and Mabs reveal subtypes of t
 A:Reference number: JH0172; MUID:90315158; PMID:2369519
 A:Accession: JH0173
 A:Molecule type: mRNA
 A:Residues: 1-511 <SCH>
 A:Cross-references: GB:X52296; NID:g63081; PIDN:CAA36544.1; PID:g63082
 A:Experimental source: brain
 A:Note: this sequence is similar to acetylcholine receptor alpha chains
 C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudod
 C:Superfamily: acetylcholine receptor
 C:Keywords: glycoprotein; transmembrane protein
 F:1-30/Domain: signal sequence #status predicted <SIG>
 F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted
 F:239-262/Domain: transmembrane #status predicted <TM1>
 F:270-288/Domain: transmembrane #status predicted <TM2>
 F:304-323/Domain: transmembrane #status predicted <TM3>
 F:479-496/Domain: transmembrane #status predicted <TM4>
 F:54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 46.5%; Score 1226.5; DB 2; Length 511;
 Best Local Similarity 46.6%; Pred. No. 1.9e-96;
 Matches 246; Conservative 75; Mismatches 134; Indels 73; Gaps 9;
 Qy 5 LAALALLPVSQGPHEKRLNALLANYNTLPRVANESPELEVRFGTLQIIDVDE 64
 Db 16 LWASLFLSFFKVSQGESORRLYRDLRLNRYNRLRPNVNDSPQIIVELQSLQIIDVDE 75
 Qy 65 KNQLITNIMLSLEWNYNLRWNSDEYGGVKDLRITPNKLNKPKDVLNYSADGFDGYQ 124
 Db 76 KNOVLITNAWLQYVWDYILSWDQYEPGVQNLRFPSQIIVPDILLYNSADERDATFH 135
 Qy 125 TNVVRSGGCLYPPGIFKSTCKMDIAWFFDDQCHDMKFGSWTYDGNOLDVLKDQAG 184
 Db 136 TNVLNVTSGGCLYPPGILKSTCIDVWFFDFQKDKFGSWTHSWGLIDLOMLE--- 192
 Qy 185 GDLSDFITNGEWYLGMPGKKNITACCPYVVDVTFIMIRRTLYFFNLVPCVLI 244
 Db 193 ADISNYSNGEMDLVGVGPKRNELYECCKEYPDVTVITIMRRTLYYGLNLLIPCVLI 252
 Qy 245 SSMAALLGFTLPDPSGEKLTGLVTLLSLTVFLNVAETLPQVSDAIPLLGTTFNCFMFW 304
 Db 253 SGLALLVFLPADSGEKISIGITVLLSLTVFVLLVAEIMPATSDSVPLTAQYFASIMIV 312
 Qy 305 ASSVVLTVVLYNYHRTADIEHMPQWIKSVFELQWLPWILRMSRPGKKTIRKTMIMNTRM 364
 Db 313 GLSVVTVVLVLFQHHDDPGGRKPKWTRILLNWCANFLMRKPGEDKVRPAQCHKPRCSL 361
 Qy 365 ELELK-----ERSKSLANVLIDDDFRHGPPPPNSTASTGNL-----GPGCSIF 410

Db 362 PLCKSYKPKHPSLKNWENVL-----PGHQPSNGNMIIYHTMENPCC--- 406
 Qy 411 RTDFRRSFVRSTMEDVGGGLG-----SHHRELHL-----ILRELQFTAR 451
 Db 407 -----PQN-NDLGSGSGKTCPLSDNEHWQKALMDTIPVIVKILEEVOFTAMR 455
 Qy 452 MKKADAEALISDWKFAAMVVDVDFLFTFTLTITATVALLSAPHII 499
 Db 456 FRKODEGEEICSEWKAFAAVIDRLCLVAFTLFAICTTILMSAPNFI 503

RESULT 8
 T25671
 hypothetical protein D2092.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T25671
 R:Gattung, S.; Maggi, L.
 submitted to the EMBL Data Library, February 1997
 A:Description: The sequence of C. elegans cosmid D2092.
 A:Reference number: Z20067
 A:Accession: T25671
 A:Status: preliminary; translated from GB/EMBL/DBBJ
 A:Molecule type: DNA
 A:Residues: 1-461 <GAT>
 A:Cross-references: EMBL:U88167; PIDN:AAB42223.1; GSPDB:GN00019; CESP:D2092.3
 A:Experimental source: strain Bristol N2; clone D2092
 C:Genetics:
 A:Gene: CESP:D2092.3
 A:Map position: 1
 A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
 C:Superfamily: acetylcholine receptor

Query Match 42.9%; Score 1132; DB 2; Length 461;
 Best Local Similarity 44.7%; Pred. No. 1.9e-88;
 Matches 216; Conservative 86; Mismatches 127; Indels 54; Gaps 6;

Qy 23 EKRLNALLANYTLERPVANSEPLEVREGLTLOQIIDVDEKNQLITNINWLSLENDY 82
 Db 26 ETKLFTLLGYNPLRPVQNSQPLEVKIKLELQQLLDVDEKNQIVSNWLSYTFWDH 85
 Qy 83 NLRNDSYGVKDLRI--TPNKLWKPDLVLYNSADEGFGTQTNTVVRSGGSLVYPP 140
 Db 86 KLQWPKYGIQIDIRPGSSDHIWKPDVLLYNLSAAEDFSTFKSNLLTYHTGTVMWIP 145
 Qy 141 GIFKSTKMDIANFPDDQDCMKFGSWYDGNLDLVKDEAGG----DLSDFITNGEW 196
 Db 146 GVLKVCOLDVTFEPDDQVCMKFGSWTFHGAIDLQIDDDTNGTQSMDLSTLYLNGEW 205
 Qy 197 YLGMFGKNTITYACCPYVDVTFIMIRRTLYFFNLIVPCVLISSMALLGFTLPP 256
 Db 206 QVISTNAKRVYSYKCCPEPYTVNYLHRRRTLYGYNLIIPSLISLMAILGFMFPP 265
 Qy 257 DSGEKLTLGVTILLSTVLNVAETLPQVSDAIPLLIGFYNCIMFWASSVVLTVVLN 316
 Db 266 DAGEKITVETILLAIIVFLISVMSEMTPTSEAVPLIGVFSCCMLWSASVYFTIWLN 325
 Qy 317 YHRTADIHEMPQWIKSVFLQWLPILRMSRPGCKITRKTIMNTRMRELELERSKSL 376
 Db 326 LHFSADSHENMPLVRVLLLEFLPWLFLMSRPGYKVK----- 363
 Qy 377 LANVLIDDDFRIGPPPNSTASTGNLPGCSTIFRTDFRSFVRPSTMEDVGGGLSHHR 436
 Db 364 -ANVIDSTDMKPKKNPLD-----CNL-----PSN-----HAGYEAQIL 397
 Qy 437 ELHLILRELOFTIARMKKADEAEALISDWKFAAMVVDVDFLFTFTIATVALLSAP 496
 Db 398 LLHSVITELRVVAFYKNEEHDRIQTDRFAAMVVDVDFLFTFTIATVALLSAP 457
 Qy 497 HII 499
 Db 458 HII 460

RESULT 9

T19862
 hypothetical protein C40C9.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 R:Hembry, C.
 submitted to the EMBL Data Library, March 1996
 A:Reference number: Z19188
 A:Accession: T19862
 A:Status: preliminary; translated from GB/EMBL/DBBJ
 A:Molecule type: DNA
 A:Residues: 1-542 <WIL>
 A:Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
 A:Experimental source: clone C40C9
 C:Genetics:
 A:Gene: CESP:C40C9.2
 A:Map position: X
 A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1;
 C:Superfamily: acetylcholine receptor

Query Match 41.0%; Score 1083.5; DB 2; Length 542;
 Best Local Similarity 42.8%; Pred. No. 3.2e-84;
 Matches 232; Conservative 86; Mismatches 152; Indels 75; Gaps 13;

Qy 10 LLALLPVSEGGPHEKRLNALLANYTLERPVANSEPLEVREGLTLOQIIDVDEKNQL 69
 Db 17 LFHLLTEVHSSADEYRLADLRHNYDPYERPVANASEPLVSVKVIYQLIILVDEKNQVI 76
 Qy 70 ITNINWLSLENDYNLNRNDSEYGVKDLRI--TPNKLWKPDLVLYNSADEGFGTQTNTV 127
 Db 77 TLVAVIEWQWTDYKLVKWPSEYGGIKDIRIPGNANAIWKPDVLLYNSADENFSTVPVY 136
 Qy 128 VYRSGGSLVYPPGIFKSTCKMDIANFPDDQDCMKFGSWYDGNLDLVKDEAGGDL 187
 Db 137 VSYTGDVLQVPPGILKLSCKIDITYFPDDQDCMKFGSWYDGNLDLVKDEAGGDL 196
 Qy 188 SD-----FITNGEWLIGMPGKNTITYACCPYVDVTFIMIRRTLYFFNLIVP 240
 Db 197 SDGIDVQYVQNGENLLAVPARHETNFD--EQYPSLFFYLLIQRRTLYGLNLIIP 254
 Qy 241 CVLISSMALLGFTLPPDSGEKLTGLVTILLSTVLNVAETLPQVSDAIPLL-----G 294
 Db 255 SFLISLTMLVGLTLPDAGEKITLITILLSVCFLSWADMTPTSEAVPLIGLIIFSG 314
 Qy 295 TYENCIMFWASSVVLTVVLNVAETLPQVSDAIPLLIGFYNCIMFWASSVVLTVVLN 354
 Db 315 AFFSCMLVSVASVTVLVLNVAETLPQVSDAIPLLIGFYNCIMFWASSVVLTVVLN 369
 Qy 355 KTMNTRMRELELERSKSLIANVLIDDDFRHGGPPPNSTASTGNLGP--GCSIFRT 412
 Db 370 KTFNCTHLKAEKAEKAKGSIKNGV-----GPGKP-----TDSVHPSGLSLMKN 416
 Qy 413 -----DFRRSF-----VRPSTN-----ED-VGGGGLSHHREL 438
 Db 417 IKLGRQOTIDFEYEFHVNHLMPVAPSEMTPRVTYSKVMAESYVEDVVMTELKYNMQA 476
 Qy 439 HLILRELOFTIARMKKADEAE--LISDWKFAAMVVDVDFLFTFTIATVALLS 494
 Db 477 CLEKNISSOTRAMRKKEEDEDEQAANDKFAAMVVDVDFLFTFTIATVALLS 536
 Qy 495 APHII 499
 Db 537 SPHLI 541

RESULT 10

T19622
 hypothetical protein C31H5.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
 C:Accession: T19622

C;Superfamily: acetylcholine receptor
 C;Keywords: neurotransmitter receptor; transmembrane protein
 F;1-28/Domain: signal sequence #status predicted <SIG>
 F;29-502/Product: nicotinic acetylcholine receptor alpha-3 chain #status predicted <MAT>

Query Match 37.2%; Score 982.5; DB 2; Length 502;
 Best Local Similarity 38.9%; Pred. No. 1.2e-75;
 Matches 199; Conservative 89; Mismatches 163; Indels 61; Gaps 5;

QY 8 LALLALLPVSEQEPHEKRLNALLANTLERPVANSEPLEVRFGTLTQOIIDVDEKQ 67
 DB LALLALLPVARASEAEHRLFERLFEDYNEIIRPVANVSDVVIHFVSSQLVKVDEVQ 76
 QY 68 LLTITNLSLEWNDYLNLRWNSDYGGVKDLRITPNKLPKDPVLMYNSADEGFGDTQTNV 127
 DB IMETNLWLKQIWDYKLNKPNPSYCGAEFRVPAEKIWPDPVLYNNVAVGDFQVDDK 136
 QY 128 VVRSGGSLVPPGIFKSTCKMDIANFPDQDCHDKMFGSWTYDGNQLDLVLKDEAGDL 187
 DB LLKTYTGEVWIPPAIFKSSCKIDVTYFPDYQNTCKMFGSWSDYDKAKIDLVLIG-SMNL 195
 QY 188 SDFITNGEWYLGMPGKKNTITYACCPPEPVVDVTFITMIRRTLYFFNLIIVPCVLIS 247
 DB KDVESGEWAIKAPGYKHDIKYNCEEYIPDITYSLYSRRLPLFTYINLIIPCLISFL 255
 QY 248 ALLGFTLPDPSGKGLTGVTLLSLVFLNVAETLPQVSDAETPLGTYFNCIMFWASS 307
 DB TVLVFVFLPSDCEGKVTLCISVLLSVFLVITETIPSTSLVIPLIGEYLLFTMIFV 315
 QY 308 VLTIVVVLNHYHTADIHMPQWIKSVFLOLWPLWRMSRPGKKIYRRTKIMMTRMLE 367
 DB IVITVFLNHYHTPTHTMPWVKTVFLNLPVFMFTRP----- 356
 QY 368 LKERSKSLIANVLIDDDFRHGPPPPPNSTASTGNL-----GPGCS----- 408
 DB -----TSNEGNAQKPRPLYCAELSNLCFSRAESKCKEYPCQDGMCGY 401
 QY 409 -----IFRTDPRSFVRPSTMEDVGG--GLGSHHRELHLILRELOFTIARMKKADEAE 461
 DB CHRRIKISNFSANLRSSESVDVAVLSALSPEIKAEIOQVSKYIAENMKRAQNEAKEI 461
 QY 462 ISDMKFAAMVDFRCLFVETLFTIATVAVLL 493
 DB QDDWKYVAMVIDRFLWVFLVETLCILGTAGLFL 493

RESULT 13
 S60589
 acetylcholine receptor alpha chain precursor - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
 C;Accession: S60589
 R;Criado, M.; Alamo, L.; Navarro, A.
 Neurochem. Res. 17, 281-287, 1992
 A;Title: Primary structure of an agonist binding subunit of the nicotinic acetylcholine
 F;1-21/Domain: signal sequence #status predicted <SIG>
 F;22-495/Product: acetylcholine receptor alpha chain #status predicted <MAT>

Query Match 36.8%; Score 970.5; DB 2; Length 495;
 Best Local Similarity 39.8%; Pred. No. 1.2e-74;
 Matches 198; Conservative 93; Mismatches 181; Indels 25; Gaps 7;

QY 5 LAALALLPVSEQEPHEKRLNALLANTLERPVANSEPLEVRFGTLTQOIIDVDE 64
 DB LRRLLLLLVPASTSDAEHRLFERLFEDYNEIIRPVANVSDVVIHFVSSQLVKVDE 66

QY 65 KNOLLITNLSLEWNDYLNLRWNSDYGGVKDLRITPNKLPKDPVLMYNSADEGFGDTQY 124
 DB VQIMETNLWLKQIWDYKLNKPNPSYDGAEEFRVPAEKIWPDPVLYNNVAVGDFQVDDK 126
 QY 125 TNVVRSGGSLVPPGIFKSTCKMDIANFPDQDCHDKMFGSWTYDGNQLDLVLKDEAG 184
 DB TRALLKTYTGEVWIPPAIFKSSCKIDVTYFPDYQNTCKMFGSWSDYDKAKIDLVLIG-SS 185
 QY 185 GDLSDFITNGEWYLGMPGKKNTITYACCPPEPVVDVTFITMIRRTLYFFNLIIVPCVLI 244
 DB MNLKDTWESGEWAIKAPGYKHDIKYNCEEYIPDITYSLYRRLPLFTYINLIIPCLLI 245
 QY 245 SSMAILGFTLPDPSGKGLTGVTLLSLVFLNVAETLPQVSDAETPLGTYFNCIMFW 304
 DB SFLTVLVFVFLPSDCEGKVTLCISVLLSVFLVITETIPSTSLVIPLIGEYLLFTMIFV 305
 QY 305 ASSVLTIVVVLNHYHTADIHMPQWIKSVFLOLWPLWRMSRPGK---KITRKTMMNT 361
 DB TLSIVITVFLNHYHTPTHTMPWVKTIIFLNLPRVFMFTRPASNEGNTQRPFPYSA 365
 QY 362 RMRELKELKERSKSLIANVLIDDDFRHGPPPPPNSTASTGNLPGCSIFR---TDFRRSF 418
 DB ELSNLNCFSRIESKVC-----KEGYP-----CQDGLCG-YCHHRAKISNFSANL 409
 QY 419 VRPSTMEDVGG--GLGSHHRELHLILRELOFTIARMKKADEAEELISDMKFAAMVYDRFC 476
 DB TRSSSESVDVAVLSALSPEIKAEIOQVSKYIAENMKRAQNEAKEIQQDMKVVAMVIDRIF 469
 QY 477 LPVFTLFTIATVAVLL 493
 DB LWFVFLVETLCILGTAGLFL 486

RESULT 14
 A24572
 nicotinic acetylcholine receptor alpha-3 chain precursor - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 08-Nov-1996
 C;Accession: A24572
 R;Boulter, J.; Evans, K.; Goldman, D.; Martin, G.; Treco, D.; Heinemann, S.; Patrick,
 Nature 319, 368-374, 1986
 A;Title: Isolation of a cDNA clone coding for a possible neural nicotinic acetylcholi
 A;Reference number: A24572; MUID:86118671; PMID:3753746
 A;Accession: A24572
 A;Molecule type: mRNA
 A;Residues: 1-499 <BOU>
 C;Superfamily: acetylcholine receptor
 C;Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra
 F;1-25/Domain: signal sequence #status predicted <SIG>
 F;26-499/Product: nicotinic acetylcholine receptor alpha chain #status predicted <MAT>

Query Match 36.8%; Score 970.5; DB 2; Length 499;
 Best Local Similarity 39.8%; Pred. No. 1.2e-74;
 Matches 199; Conservative 91; Mismatches 180; Indels 33; Gaps 7;

QY 3 PMLAALALLPVSEQEPHEKRLNALLANTLERPVANSEPLEVRFGTLTQOIIDV 62
 DB PLSMLMLVLMPLPAASASEAHLFOYLFEDYNEIIRPVANVSHPIVIOFEVMSQLVKV 68
 QY 63 DEKNOLLITNLSLEWNDYLNLRWNSDYGGVKDLRITPNKLPKDPVLMYNSADEGFGDT 122
 DB DEVNQIMETNLWLKQIWDYKLNKPNPSYDGAEEFRVPAEKIWPDPVLYNNVAVGDFQVD 128
 QY 123 YQTNVVRSGGSLVPPGIFKSTCKMDIANFPDQDCHDKMFGSWTYDGNQLDLVLKDE 182
 DB DKTALLKTYTGEVWIPPAIFKSSCKIDVTYFPDYQNTCKMFGSWSDYDKAKIDLVLIG- 187
 QY 183 AGGDLSDFITNGEWYLGMPGKKNTITYACCPPEPVVDVTFITMIRRTLYFFNLIIVPCV 242
 DB SSMNLKDYWESGEWAIKAPGYKHDIKYNCEEYIPDITYSLYRRLPLFTYINLIIPCL 247
 QY 243 LISSMAILGFTLPDPSGKGLTGVTLLSLVFLNVAETLPQVSDAETPLGTYFNCIMF 302

Db 248 LISFLVLYFLPSDCGKVTLCISVLLSTVFLVITETISTVSLVPLIGEYLLFTMI 307
QY 303 MVASSVLTAVVLYNYHRTADIHMPQWIKSVFLOLWILRMSRP--GKKITRKT-IMM 359
Db 308 FVTLISVIVFVNLVHVRPTTHTMTWKAFLNLLPRVMTPTSGEGDTPKTRTEV 367
QY 360 NTRMRLELKERSSKLLANVLDDDDFRHGPP-----PNSTASTGNLGPCCSIFKT 412
Db 368 GAELSNNLNCFSRCLQKLOGLR-----PLPRWDLMLPHRRYKISN-----408
QY 413 DFRRSFVRPSTMEDVGG--GLGSHRHLEHLILRELOFITARMKKADEEAEELISDWKFAAM 470
Db 409 -FSANTRSSSSSVNAVLSLSALSPKIKRATOSVYIAENMKAAQNAVEIQDDWKYVAM 467
QY 471 VDRFCLFVFTFTIATVAVLL 493
Db 468 VIDRIFLWFLVILCGLTAGLFL 490

RESULT 15
ACFPAL
nicotinic acetylcholine receptor alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jun-2002
C:Accession: S00381; A38801
R:Bossy, B.; Ballivet, M.; Spierer, P.
EMBO J. 7, 611-618, 1988
A:Title: Conservation of neural nicotinic acetylcholine receptors from Drosophila to vertebrates
A:Reference number: S00381; MUID:88283626; PMID:2840281
A:Accession: S00381
A:Molecule type: DNA
A:Residues: 1-567 <BOS>
A:Cross-references: GB:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A:Note: 538-Tyr was also found
C:Genetics:
A:Gene: FlyBase:nACR-alpha-96Aa
A:Cross-references: FlyBase:FBgn0000036
A:Map position: 3R 96A
A:Introns: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-567/Product: nicotinic acetylcholine receptor alpha-like chain #status predicted <M>
F:22-240/Domain: extracellular #status predicted <EXT>
F:240-264/Domain: transmembrane #status predicted <TM1>
F:272-290/Domain: transmembrane #status predicted <TM2>
F:306-325/Domain: transmembrane #status predicted <TM3>
F:326-513/Domain: intracellular #status predicted <INT>
F:514-532/Domain: transmembrane #status predicted <TM4>
F:45, 233/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:149-163,222-223/Disulfide bonds: #status predicted

Query Match 36.5%; Score 964.5; DB 1; Length 567;
Best Local Similarity 36.5%; Pred. No. 4.8e-74;
Matches 198; Conservative 95; Mismatches 158; Indels 91; Gaps 9;

QY 21. PHEKRLNALLANVTLEPVPANSEPLEVRFGLTLOQIIDVDEKNOLLITNIWLSLEWN 80
Db 23. PDARKLYDDLSNRYLIRPVGNNSDRLTVMKGLRISOLIDVNLKNOIMTNNVWVEQWN 82
QY 81. DYNLRWNDSEYGGKDLRITPKLWKPDVLMYNSADEGFGCTGYQTNVVRSGGSLYVPP 140
Db 83. DYKLKWNPDYGGVDTLVHPSEHLVHPDVLVYNNADNGYEVTIMTKAILHHHTGKVVWKP 142
QY 141. GIFKSTCKMDIAWPFDDQHCMDKFGSWTYDGNOLDL-VLKD-----EAGGDLSDFIT 192
Db 143. AIYKSFCEIDVEYFPDEQTCFMKFGSWTYDGYWVLDRLHLKQTADSDNIEVGIDLDQYI 202

QY 193 NGEWYLIGMPGKKNTITYACCPPEYVDVFTTMRRTLYFFNLIVPCVLISSMALLGF 252
Db 203 SVENDIMRPVARNKRYFSCCEPYLDIVFNLTLRKTLFTVNLIIPCVGISFLSVLF 262
QY 253 TLPPDSGEKLTGVTILLSLTVFLNVAETLPOVSDAIPLLGYFNCIMFMASSVVLTV 312
Db 263 YLPSSDSGEKISLCISILLSTVFFLLAEIIPPTSLSVPLLGKYLFTMMLVTLSSVVVTI 322
QY 313 VVLYNYHRTADIHMPQWIKSVFLOLWILRMSRPCKKITRKTIMNTRMRELEKERS 372
Db 323 AVLNVNFRSPVTHRMAPVWORFIQILPKLLCIERPKKE-----EPEEDQ 367
QY 373 SKSLLANVL-----DID-----DDFRHG-----pppp 394
Db 368 PPEVLTDVYHLPPDVVKFVNYDSKRSFGDYGIPALPASHREFDLAAAGGISAHCFAPPLP 427
QY 395 NS-----TASTGNLGPCC-----SIFRTDFRRSFVRPSTMEDVGGGLSHHR 436
Db 428 SSLPLPGADDDLFSPSGLNGDISPGCCPAAAAAADLSPTFEKP-----YAR 475
QY 437 ELHLILRELOFITARMKKADEEAEELISDWKFAAMVVDRECLFVFTLTIIATVAVLLSAP 496
Db 476 EMEKTTIEGSRFIAQHVKNKDKFESVEDMKYVAMVLDRMFLWIFATACVVGVTALIILOAP 535
QY 497 HI 498
Db 536 SL 537

Search completed: August 13, 2003, 15:30:22
Job time : 19.7131 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:30 ; Search time 43.9474 Seconds
(without alignments)
1809.483 Million cell updates/sec

Title: US-09-303-232-6
Perfect score: 2640
Sequence: 1 MAPMLAALALLPVSQ.....LFTIATVALLSAPHIIVQ 501

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
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12: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
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22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2640	100.0	501	21	AA50816	H. virescens acety
2	1803.5	68.3	496	21	AA50815	H. virescens acety
3	1609	60.9	770	21	AA50814	D. melanogaster ac
4	1570.5	59.5	498	22	ABB60432	Drosophila melanog
5	1283	48.6	311	22	ABB63683	Drosophila melanog
6	1258.5	47.7	502	15	AAW4153	Human neuronal nic
7	1258.5	47.7	502	18	AAW09025	Neuronal nicotinic
8	1258.5	47.7	502	21	AAW24088	Human PRO2145 prot
9	1258.5	47.7	502	22	AAW24088	Nicotinic acetylch

10	1258.5	47.7	502	22	AAW50012	Wild-type human al
11	1258.5	47.7	502	23	ABB82435	Human neuronal NAC
12	1258.5	47.7	502	23	ABG70492	Human neuronal nic
13	1254.5	47.5	502	19	AAW69216	V274T variant huma
14	1253	47.5	502	18	AAW12368	Neuronal alpha-bun
15	1252.5	47.4	502	22	AAW50015	Mutant human alpha
16	1248.5	47.3	502	22	AAW50016	Mutant human alpha
17	1242.5	47.1	502	22	AAW50017	Mutant human alpha
18	1226.5	46.5	511	18	AAW12369	Neuronal alpha-bun
19	1080	40.9	554	22	AAE12824	Caenorhabditis ele
20	1080	40.9	554	24	ABP96318	Caenorhabditis ele
21	989.5	37.5	504	18	AAW09022	Neuronal nicotinic
22	962.5	36.5	470	22	AAW50014	Chimeric alpha7/5-
23	946.5	35.9	504	23	ABB82431	Human neuronal NAC
24	946.5	35.9	504	23	ABG70488	Human neuronal nic
25	943	35.7	576	22	ABB61954	Drosophila melanog
26	942	35.7	448	22	AAW50018	Mature cell surfac
27	940.5	35.6	504	15	AAW44156	Human neuronal nic
28	933	35.3	494	18	AAW09018	Neuronal nicotinic
29	933	35.3	494	23	ABB82434	Human neuronal NAC
30	933	35.3	494	23	ABG70491	Human neuronal nic
31	933	35.3	580	22	ABB62727	Drosophila melanog
32	922.5	34.9	529	15	AAW44155	Human neuronal nic
33	922.5	34.9	529	16	AAW73966	Alpha 2 subunit of
34	922.5	34.9	529	18	AAW09021	Neuronal nicotinic
35	922.5	34.9	529	23	ABB82430	Human neuronal NAC
36	922.5	34.9	529	23	ABG31800	Human neuronal nic
37	922.5	34.9	529	23	ABG61850	Prostate cancer-as
38	922	34.9	479	22	AAE12823	Caenorhabditis ele
39	922	34.9	479	24	ABP96317	Caenorhabditis ele
40	918.5	34.8	631	23	AAO17243	Modified acetylcho
41	915	34.7	622	23	AAO17245	Modified acetylcho
42	915	34.7	622	23	ABB08885	Modified hen ACR s
43	910.5	34.5	495	11	AAW07143	Neuronal nicotinic
44	908.5	34.4	519	22	ABB62694	Drosophila melanog
45	906	34.3	552	22	ABB61667	Drosophila melanog

ALIGNMENTS

RESULT 1
AA50816
ID AA50816 standard; Protein; 501 AA.
XX
AC AA50816;
XX
DT 17-FEB-2000 (first entry)
XX
DE H. virescens acetyl-choline receptor protein from clone Hva7-2.
XX
DE DE19819829-AL.
XX
KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
KW neurotransmission; plant protection agent; conductance; AChR.
XX
OS Heliothis virescens.
XX
PN DE19819829-AL.
XX
PD 11-NOV-1999.
XX
PF 04-MAY-1998; 98DE-1019829.
XX
PR 04-MAY-1998; 98DE-1019829.
XX
PA (FARB) BAYER AG.
XX
PI Adamczewski M, Oellers N, Schulte T;
XX
DR WPI; 2000-014207/02.
XX
PT New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides

XX Example 1a; Page 22-23; 26pp; German.
 XX This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides; or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence represents an
 CC acetyl-choline receptor isolated from *Heliothus virescens*.
 XX SQ Sequence 501 AA;

Query Match 100.0%; Score 2640; DB 21; Length 501;
 Best Local Similarity 100.0%; Pred. No. 5.9e-270;
 Matches 501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 MAPMLAALALLPVSPGPHKRLNALLANTLERPVANSEPLEVRFGLTLOQII 60
 Db 1 MAPMLAALALLPVSPGPHKRLNALLANTLERPVANSEPLEVRFGLTLOQII 60
 Oy 61 DVDEKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLNKDPVLMYNSADEGFD 120
 Db 61 DVDEKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLNKDPVLMYNSADEGFD 120
 Oy 121 GTYQTNVVRSGGSLVPPGIFKSTCKMDIAWPFDDQHCMDKFGSWTYDGNLDLVK 180
 Db 121 GTYQTNVVRSGGSLVPPGIFKSTCKMDIAWPFDDQHCMDKFGSWTYDGNLDLVK 180
 Oy 181 DEAGDLSDFITNGEWYLGMPGKNTITYACCPYVDVFTTIRRTLYFFNLIVP 240
 Db 181 DEAGDLSDFITNGEWYLGMPGKNTITYACCPYVDVFTTIRRTLYFFNLIVP 240
 Oy 241 CVLISSMALLGFTLPDPSGKLTGLVITLLSLTFLNLVAETLPQVSDAIPLLGYFNCI 300
 Db 241 CVLISSMALLGFTLPDPSGKLTGLVITLLSLTFLNLVAETLPQVSDAIPLLGYFNCI 300
 Oy 301 MFVASSVVLTVVVLNYHHRHTADHEMPQWIKSFLOWLWILRMSRPGKTKITRMN 360
 Db 301 MFVASSVVLTVVVLNYHHRHTADHEMPQWIKSFLOWLWILRMSRPGKTKITRMN 360
 Oy 361 TRMRELEKRSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFRSEVR 420
 Db 361 TRMRELEKRSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFRSEVR 420
 Oy 421 PSTMEDVGGGLGSHHRELHLILRELQFTARMKKADEAEELISDWKFAAMVVDRECLFV 480
 Db 421 PSTMEDVGGGLGSHHRELHLILRELQFTARMKKADEAEELISDWKFAAMVVDRECLFV 480
 Oy 481 TLFITTIATVALLSAPHIIVQ 501
 Db 481 TLFITTIATVALLSAPHIIVQ 501

RESULT 2
 AAY50815
 ID AAY50815 standard; Protein; 496 AA.
 XX AC AAY50815;
 XX DT 17-FEB-2000 (first entry)
 XX DE H. *virescens* acetyl-choline receptor protein from clone Hva7-1.
 XX KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 XX OS neurotransmission; plant protection agent; conductance; AChR.
 XX OS *Heliothus virescens*.

PN DEL9819829-AL.
 XX 11-NOV-1999.
 XX 04-MAY-1998; 98DE-1019829.
 XX 04-MAY-1998; 98DE-1019829.
 XX (FARB) BAYER AG.
 XX Adamczewski M, Oellers N, Schulte T;
 XX WPI; 2000-014207/02.
 XX N-PSDB; AAZ24476.
 XX New nucleic acid encoding a nicotinic acetylcholine receptor from
 XX insects, used to identify potential insecticides
 XX Example 1a; Page 17-19; 26pp; German.
 XX This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides; or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence represents an
 CC acetyl-choline receptor isolated from *Heliothus virescens*.
 XX SQ Sequence 496 AA;

Query Match 68.3%; Score 1803.5; DB 21; Length 496;
 Best Local Similarity 68.7%; Pred. No. 1.9e-181;
 Matches 347; Conservative 53; Mismatches 78; Indels 27; Gaps 7;
 Oy 2 APMLAALALLPVSEQ-GPHEKRLNALLANTLERPVANSEPLEVRFGLTLOQII 60
 Db 12 APGLLLLLCLLWPRGARGCYHEKRLHLLHDHYNLVRPVPVNESDPLQLSGLTLMQII 71
 Oy 61 DVDEKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLNKDPVLMYNSADEGFD 120
 Db 72 DVDEKNOLLITNIWLSLEWNDYNLRWNDSEYGGVKDLRITPNKLNKDPVLMYNSADEGFD 131
 Oy 121 GTYQTNVVRSGGSLVPPGIFKSTCKMDIAWPFDDQHCMDKFGSWTYDGNLDLVK 180
 Db 132 STYPTNVVRNNGSLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGLDLQLQ 191
 Oy 181 DEAGDLSDFITNGEWYLGMPGKNTITYACCPYVDVFTTIRRTLYFFNLIVP 240
 Db 192 DEGGDISSFVTNGEWELIGVPGGRNEIYNCCPEYIDITFAVIRKTKLYFFNLIVP 251
 Oy 241 CVLISSMALLGFTLPDPSGKLTGLVITLLSLTFLNLVAETLPQVSDAIPLLGYFNCI 300
 Db 252 CVLISSMALLGFTLPDPSGKLTGLVITLLSLTFLNLVAETLPQVSDAIPLLGYFNCI 311
 Oy 301 MFVASSVVLTVVVLNYHHRHTADHEMPQWIKSFLOWLWILRMSRPGKTKITRMN 360
 Db 312 MFVASSVVLTVVVLNYHHRHTADHEMPQWIKSFLOWLWILRMSRPGKTKITRMN 370
 Oy 361 TRMRELEKRSKSLANVLIDDDFRHGPPPPNSTASTGNLPGGCSIFRTDFRSEVR 420
 Db 371 PPPDLELRERSKSLANVLIDDDFRH-----PQAQO-----PQCCRY---YRGG--- 414
 Oy 421 PSTMEDVGGGLGSH-----HRELHLILRELQFTARMKKADEAEELISDWKFAAMVVDRE 475
 Db 415 -----EENGAGLAHSCFGVDYELSLILKEIRVITQDMRKDDDEDADISDWKFAAMVVDRL 470
 Oy 476 CLFVFTLTITTIATVALLSAPHIIV 500
 Db 471 CLIFTTITTIATVALLSAPHIIV 495

Query Match	59.5%	Score 1570.5;	DB 22;	Length 498;
Best Local Similarity	61.1%;	Pred. No. 8.6e-157;		
Matches 319:	Conservative 44;	Mismatches 84;	Indels 75;	Gaps 9

FT Domain 318..461
 FT /label= cytoplasmic_loop
 FN WO9420617-A2.
 XX 15-SEP-1994.
 XX 08-MAR-1994; 94WO-US02447.
 XX 08-MAR-1993; 93US-0028031.
 XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 PA (SIBI-) SIBIA NEUROSCIENCES INC.
 XX Elliott KJ, Ellis SB, Harpold MM;
 XX WPI; 1994-303024/37.
 DR N-PSDB; AAV12197.
 XX Human neuronal nicotinic acetylcholine receptor subunits and DNA -
 PT also transformed cells useful for screening cpds. which modulate
 PT activity of the receptor
 XX
 XX Claim 7; Page 80-81; 99pp; English.
 PS
 CC The present sequence represents a human neuronal nicotinic acetylcholine
 CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta
 CC NACHR subunits may be used in a method of screening compounds to
 CC identify any which modulate the activity of human neuronal NACHR.
 CC Subunit specific antibodies may be used to monitor the distribution
 CC and expression density of various subunits in normal vs diseased brain
 CC tissues. Testing of single receptor subunits or specific receptor
 CC subunit combinations with a variety of potential agonists or antagonists
 CC provides information with respect to the function and activity of the
 CC individual subunits and should lead to the identification and design of
 CC compounds that are capable of very specific interaction with one or
 CC more receptor subtypes. The resulting drugs should exhibit fewer
 CC unwanted side effects than drugs identified e.g. screening with cells
 CC that express a variety of subtypes.
 XX
 SQ Sequence 502 AA;
 Query Match 47.7%; Score 1258.5; DB 15; Length 502;
 Best Local Similarity 48.6%; Pred. No. 9e-124;
 Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;
 QY 8 LALLA-LLPVSEOGPEKRLNALLANYNTERPVAENSEPLEVRGLTQIIVDEKN 66
 DB 10 LALAASLLHVSLOGEFQRLKLYELVKNYPLRPVANDSQPLTVYFSLQLQIMDVDEKN 69
 QY 67 QLLITNIWLSLENDYNLNRNDSEYGVKDLRTTPNKLKMPDVLYMNSADEGFDGTYQTN 126
 DB 70 QVLTNIWLQMSWTDHYLQWNSYEPGVKTVPDPGQIWKPDILLYNSADERDAFFHN 129
 QY 127 VVVRSGSCLYVPPGIFKSTCKMDIAWFFPDQHCCKFGSWYDGNQLDLVLKDBAGD 186
 DB 130 VLNVSSGHCOYLPPIGFKSCYIDVRWFFDVQHCKLFGSWYDGNQLDLVLKDBAGD 186
 QY 187 LSDFITNGEWYLGMPGKNTITYACCPYVDVTFIMIRRTLYFFNLIIVPCVLISS 246
 DB 187 ISGYINGEWDLVIGFGKSEREYCEKPEYDPDVTFTVTRRTLYGNNLLIPCVLISA 246
 QY 247 MALLGTLPPDSGEKITLGVTILLSTVFLNLVAETLPQVSDAIPLLGYFNCIMPMVAS 306
 DB 247 LALLVLLPADSGEKISLGTIVLLSTVFMLLVAEIMPATSDSVPLIAQYFASTMIIVGL 306
 QY 307 SVVLTVVVLYNHHRTADIEMPOWIKSVFLOLWPLWLRSPGKKITRKTIMNTRMREL 366
 DB 307 SVVTVIVLYQHHDDGGKMPKRWTRVILLNCAWFLMKRPGEDKVRPACQHKQRCSL 366
 QY 367 ELKERSKSLANVLDDDFRHGPPPNSTASTGNL-----GPGC 407
 DB 367 ASVEMSAV-----PPP-----ASNGNLLYIGRGLDGVHCVTPDPDSGVVC 407

QY 408 SIFRTDFRRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFTIARMKKADEAEELISDW 465
 DB 408 G-----RMACSPTHDEHLLHGGOPPEGDPDLAKILEEVRYIANFRQDESEAVCSEW 460
 QY 466 KFAAMVVDRECLFVFTLTIIATVAVLLSAPHII 499
 DB 461 KFAACVVDRLCLMAFSVFTIICTIGILMSAPNEV 494

RESULT 7

AAW09025
 ID AAW09025 standard; Protein; 502 AA.

XX AAW09025;

DT 09-APR-1997 (first entry)

XX Neuronal nicotinic acetylcholine receptor alpha-7 subunit.

DE Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;
 KW ligand-gated receptor.

XX Homo sapiens.

XX WO9641876-A1.

XX 27-DEC-1996.

PF 07-JUN-1996; 96WO-US09775.

XX 07-JUN-1995; 95US-0484722.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Elliott KJ, Harpold MM;

XX WPI; 1997-065463/06.

DR N-PSDB; AAT48239.

XX Nucleic acids encoding nicotinic acetylcholine receptor sub-units -
 PT used in screening to determine the effect of drugs on the receptor

PS Disclosure; Page 73-74; 108pp; English.

XX The alpha-7 subunit (AAW09025) of the human neuronal nicotinic
 CC acetylcholine receptor (nAChR) can be expressed in transfected
 CC host cells carrying alpha-7 subunit DNA (see also AAT48239). Host
 CC cells, esp. mammalian cells or amphibian oocytes, expressing the
 CC recombinant alpha-7 subunit, opt. in combination with other
 CC recombinant alpha and/or beta subunits (see also AAW09018-24,
 CC AAW09026-27), can be used to examine the function of human AChR and
 CC to identify cpds. that modulate its activity.

XX Sequence 502 AA;

Query Match 47.7%; Score 1258.5; DB 18; Length 502;
 Best Local Similarity 48.6%; Pred. No. 9e-124;
 Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;

QY 8 LALLA-LLPVSEOGPEKRLNALLANYNTERPVAENSEPLEVRGLTQIIVDEKN 66
 DB 10 LALAASLLHVSLOGEFQRLKLYELVKNYPLRPVANDSQPLTVYFSLQLQIMDVDEKN 69
 QY 67 QLLITNIWLSLENDYNLNRNDSEYGVKDLRTTPNKLKMPDVLYMNSADEGFDGTYQTN 126
 DB 70 QVLTNIWLQMSWTDHYLQWNSYEPGVKTVPDPGQIWKPDILLYNSADERDAFFHN 129
 QY 127 VVVRSGSCLYVPPGIFKSTCKMDIAWFFPDQHCCKFGSWYDGNQLDLVLKDBAGD 186
 DB 130 VLNVSSGHCOYLPPIGFKSCYIDVRWFFDVQHCKLFGSWYDGNQLDLVLKDBAGD 186
 QY 187 LSDFITNGEWYLGMPGKNTITYACCPYVDVTFIMIRRTLYFFNLIIVPCVLISS 246

Db' 187 ISGYPNGEWDLVGIPIKRSERFECCKEYPPDVTFTVWRRRTLYLGLNLLIPCVLISA 246
 Qy 247 MALLGFTLPDPSGKFLGVTILSLVFLNLVAETLPQVSDAIPGLGTYFNCIMFVWAS 306
 Db 247 LALLVFLPADSGEKISLGITVLLSVFLNLVAEIMPATSDSVPLIAQYFASFTMIIVGL 306
 Qy 307 SVLVTVVVLNHHRTADIHEMPQWIKSVFLOLWPILMRSPGKKITRKTMMTRREL 366
 Db 307 SVVTVTVLQYHHDDPDGKMPKTRVILLNWCWFLMRKRPGEKVRPACQHKQRCSL 366
 Qy 367 ELKERSKSLLANVLDIDDDFRHGPDPNPNSTASTGNL-----GPGC 407
 Db 367 ASVEMSAVA-----PPP-----ASGNLLYIGFGLDGVCHVCPDPSGVC 407
 Qy 408 SIERTDPRRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEAEELISDW 465
 Db 408 G-----RMACSPTHDEHLHGQPPGDPDLAKILEEVRYIANFRQCDESEAVCSEW 460
 Qy 466 KFAAMVVDRLCLFVFTLTFTTIATVAVLLSAPHII 499
 Db 461 KFAACVVDRLCLMAFSVFTIITIGILMSAPNFV 494

RESULT 8

AAB24088

ID AAB24088 standard; Protein; 502 AA.

XX

AC AAB24088;

XX

XX 29-JAN-2001 (first entry)

XX

DE Human PRO2145 protein sequence SEQ ID NO:77.

XX

Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
 proliferation; tumorigenesis; identification; cancer; cytostatic;
 KW neutropic; neuroprotective; antiinflammatory; immunosuppressive;
 KW immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
 KW neuronal disorder; glioma disorder; astrocytic disorder; angiogenic;
 KW hypothalamic disorder; glandular disorder; macrophagal disorder;
 KW epithelial disorder; stromal disorder; blastocoeleic disorder;
 KW inflammatory disorder; immunologic disorder.

XX Homo sapiens.

OS

XX WO200053755-A2.

XX

XX 14-SEP-2000.

XX

XX 06-JAN-2000; 2000WO-US00376.

XX

XX 08-MAR-1999; 99WO-US05028.

XX 02-JUN-1999; 99WO-US12252.

XX 23-JUN-1999; 99US-0141037.

XX 07-JUL-1999; 99US-0143048.

XX 26-JUL-1999; 99US-0145698.

XX 30-NOV-1999; 99WO-US28313.

XX 20-DEC-1999; 99WO-US30911.

XX 05-JAN-2000; 2000WO-US00219.

XX (GETH) GENENTECH INC.

XX

XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;

XX Watanabe CK, Wood WI;

XX

XX WPI; 2000-572270/53.

XX N-PSDB; AAC58395.

XX

XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
 XX treatment, diagnosis and prevention of cancer -
 XX

XX Claim 61; Fig 58; 286pp; English.

XX

XX

XX

XX

XX

XX

XX

XX

CC The present invention describes an isolated antibody that binds to
 CC one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO355,
 CC PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
 CC PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
 CC PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
 CC PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
 CC growth. The PRO polypeptides and nucleotides are useful in the
 CC treatment, diagnosis and prevention of cancer. The antibodies and other
 CC anti-tumour compounds may be used to treat various conditions, including
 CC those characterised by overexpression and/or activation of the amplified
 CC PRO genes. Exemplary conditions or disorders to be treated with such
 CC antibodies and other compounds include benign or malignant tumours
 CC (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
 CC colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
 CC carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
 CC leukaemias and lymphoid malignancies, other disorders such as neuronal,
 CC glioma, astrocytic, hypothalamic and other glandular, macrophagal,
 CC epithelial, stromal and blastocoeleic disorders, and inflammatory,
 CC angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
 CC primers and hybridisation probes used in the isolation of the human PRO
 CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
 CC PRO polynucleotide and protein sequences given in the exemplification of
 CC the present invention.

XX

SQ Sequence 502 AA;

Query Match 47.7%; Score 1258.5; DB 21; Length 502;

Best Local Similarity 48.6%; Pred. No. 9e-124;

Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;

Qy 8 LALLA-LLPVSEQEPHEKRLNLLNANTLERPVANSEPLEVRFGLTQQIIVDDEKN 66

Db 10 LALAASLLHVSLOGEFQKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIMDVDEKN 69

Qy 67 QLITITNWLSEWYDYNLWNSDSEYGVGKDLRITPNKWKPDVLYMNSADEGDTGYQTN 126

Db 70 QVLTNTNWLQMSWTDHVLQNVSEYPCVKTVPDQGIWKPDILLYNSADERDATHFN 129

Qy 127 VVVRSGSCLYVPPGIFKSKMDIAWFPDDOHCMDKMGFSGWYDGNLDLVLKDEAGD 186

Db 130 VLVNSSGHCOYLPPIGIFKSCYIDVRWFPDQVQCKLFGSGWSYGGWSLDQMOE---AD 186

Qy 187 LSDFITNGEWYLGMPGKKNITVYACCPYVDVDTFTIMIRRTLYYFFNLVPCVLIS 246

Db 187 ISGYPNGEWDLVGIPIKRSERFECCKEYPPDVTFTVWRRRTLYLGLNLLIPCVLISA 246

Qy 247 MALLGFTLPDPSGKFLGVTILSLVFLNLVAETLPQVSDAIPGLGTYFNCIMFVWAS 306

Db 247 LALLVFLPADSGEKISLGITVLLSVFLNLVAEIMPATSDSVPLIAQYFASFTMIIVGL 306

Qy 307 SVLVTVVVLNHHRTADIHEMPQWIKSVFLOLWPILMRSPGKKITRKTMMTRREL 366

Db 307 SVVTVTVLQYHHDDPDGKMPKTRVILLNWCWFLMRKRPGEKVRPACQHKQRCSL 366

Qy 367 ELKERSKSLLANVLDIDDDFRHGPDPNPNSTASTGNL-----GPGC 407

Db 367 ASVEMSAVA-----PPP-----ASGNLLYIGFGLDGVCHVCPDPSGVC 407

Qy 408 SIERTDPRRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARMKKADEAEELISDW 465

Db 408 G-----RMACSPTHDEHLHGQPPGDPDLAKILEEVRYIANFRQCDESEAVCSEW 460

Qy 466 KFAAMVVDRLCLFVFTLTFTTIATVAVLLSAPHII 499

Db 461 KFAACVVDRLCLMAFSVFTIITIGILMSAPNFV 494

RESULT 9

AAB24088

ID AAB24088 standard; Protein; 502 AA.

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XX Special cell culture medium for treating cells and for inducing
PT mammalian cell lines to conduct calcium ions, comprising specified
PT concentrations of ions of sodium, calcium and potassium at specified pH
PT
XX
PS Disclosure; Pages 61-63; 77pp; English.

XX The present sequence is wild-type human alpha7 nicotinic acetylcholine
CC gated ion channel. The human alpha7 ion channel was used in the
CC construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
CC gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
CC ion channel can be expressed by recombinant cells in the present
CC invention, resulting in preferential calcium ion conductance by the
CC cells.

XX
SQ Sequence 502 AA;

Query Match 47.7%; Score 1258.5; DB 22; Length 502;
Best Local Similarity 48.6%; Pred. No. 9e-124;
Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;

QY 8 LALLA-LLPVSQGPHEKRLNALLANYTLERPVANESPELEVRFGTLTQOIIDVDEKN 66
DB 10 LALAASLLHVSLOQEFORKLYKELVKNYPLERPVANDSPLTYVFSLSLLQIMDVDEKN 69

QY 67 QLLTITNLSLEWNYNLRWNSDEYGGVKDLRITPNKLWPDVLYMNSADEGFDGTOTN 126
DB 70 QVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVRFPPDGOIKWPKDILLYNSADERFDEFTN 129

QY 127 VVVRSGSCLYVPPGIEFKSTCKMDIANFPDDQHCDFKGSWTDYDGNLDLVKDEAGD 186
DB 130 VLVNSSGHCQYLPPIGFKSCYIDVRWFPDQVHCKLKFGWSYGGWSLDLQMOE---AD 186

QY 187 LSDFITNGEWLYIGMPGKKNITVACCPPEPVVDVFTTIRMIRRTLYFFNLIVPCVLIS 246
DB 187 ISGYIPNGEWDLVGIPKRSERFECCKEYPDVFTVTHRRRTLYGLNLLIPCVLISA 246

QY 247 MALLGFTLPDPSGKGLTGVITLLSLVFLNVAETLPQVSDAIPDLGTYNCFIMFVAS 306
DB 247 LALLVFLPADSGEKISLGITVLLSLVFLNVAEIMPATSDSVPLIAQVFASTMIIVGL 306

QY 307 SVVLTVVVLYNHHRTADIEHMPQWIKSVFLOLWLPILRMSRPGKIKTRKTMNTRREL 366
DB 307 SVVTVTVLQYHHHDPOGGMKPKWTRVILLNWCALFLMRKRPGEKDKVRPACQHKQRCSL 366

QY 367 ELKERSKSLANVLDIDDDFRHGPPPPNSTASTGNL-----ASGNLLYIGFRLDGVHCVPTPDSGVVC 407
DB 367 ASVEMSAVA-----PPP-----ASGNLLYIGFRLDGVHCVPTPDSGVVC 407

QY 408 SIFRTDPRFRSVRSTMEDV---GGGLGSHHRELHLILRELQFIFARMKKADEAEELISDW 465
DB 408 G-----RMACSPTHDEHLHGQPPGDPDLAKILEEVRYIANRFRCDSEAVCSEW 460

QY 466 KFAAMVDRFCFLFTFTIATVALLSAPHII 499
DB 461 KFAACVDRICLMAFSVFTICTIGILMSAPNFV 494

RESULT 11
ABB82435
ID ABB82435 standard; Protein; 502 AA.

XX
AC ABB82435;
XX
DT 22-JAN-2003 (first entry)
XX
DE Human neuronal NACHr alpha7 subunit.
XX
KW Human; neuronal; nicotinic acetylcholine receptor; NACHr; drug screening;
KW immunochemistry; NACHr alpha7 subunit; receptor.
XX
OS Homo sapiens.

XX WO200259266-A2.
XX 01-AUG-2002.
XX 29-OCT-2001; 2001WO-US50985.
XX 01-NOV-2000; 2000US-0703951.
XX (MERI) MERCK & CO INC.
XX Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KI;
XX WPI; 2002-698532/75.
XX N-PSDB; ABV73248.

XX Cell comprising nucleic acids encoding human alpha and beta subunits of
PT neuronal nicotinic acetylcholine receptors, useful for in vitro
PT screening of a drug substance in a test system specific for humans
XX Examples; Page 130-131; 143pp; English.

XX The invention relates to a suitable host cell transfected with an
CC isolated nucleic acid molecule comprising a sequence of nucleotides or
CC ribonucleotides that encodes at least one alpha or beta subunit of a
CC human neuronal nicotinic acetylcholine receptor (NACHr). The compositions
CC and methods of the present invention, which provide a means to prepare
CC synthetic or recombinant receptors and receptor subunits that are
CC substantially free of contamination from many other receptor proteins,
CC are useful for observing the effect of a drug substance on a particular
CC subtype to perform in vitro screening of the drug substance in a test
CC system that is specific for humans. The antibodies can be used in
CC immunochemistry and for diagnostic and therapeutic applications. The
CC present sequence represents a human neuronal NACHr alpha7 subunit.

XX Sequence 502 AA;

Query Match 47.7%; Score 1258.5; DB 23; Length 502;
Best Local Similarity 48.6%; Pred. No. 9e-124;
Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;

QY 8 LALLA-LLPVSQGPHEKRLNALLANYTLERPVANESPELEVRFGTLTQOIIDVDEKN 66
DB 10 LALAASLLHVSLOQEFORKLYKELVKNYPLERPVANDSPLTYVFSLSLLQIMDVDEKN 69

QY 67 QLLTITNLSLEWNYNLRWNSDEYGGVKDLRITPNKLWPDVLYMNSADEGFDGTOTN 126
DB 70 QVLTNTIWLQMSWTDHYLQWNVSEYPGVKTVRFPPDGOIKWPKDILLYNSADERFDEFTN 129

QY 127 VVVRSGSCLYVPPGIEFKSTCKMDIANFPDDQHCDFKGSWTDYDGNLDLVKDEAGD 186
DB 130 VLVNSSGHCQYLPPIGFKSCYIDVRWFPDQVHCKLKFGWSYGGWSLDLQMOE---AD 186

QY 187 LSDFITNGEWLYIGMPGKKNITVACCPPEPVVDVFTTIRMIRRTLYFFNLIVPCVLIS 246
DB 187 ISGYIPNGEWDLVGIPKRSERFECCKEYPDVFTVTHRRRTLYGLNLLIPCVLISA 246

QY 247 MALLGFTLPDPSGKGLTGVITLLSLVFLNVAETLPQVSDAIPDLGTYNCFIMFVAS 306
DB 247 LALLVFLPADSGEKISLGITVLLSLVFLNVAEIMPATSDSVPLIAQVFASTMIIVGL 306

QY 307 SVVLTVVVLYNHHRTADIEHMPQWIKSVFLOLWLPILRMSRPGKIKTRKTMNTRREL 366
DB 307 SVVTVTVLQYHHHDPOGGMKPKWTRVILLNWCALFLMRKRPGEKDKVRPACQHKQRCSL 366

QY 367 ELKERSKSLANVLDIDDDFRHGPPPPNSTASTGNL-----ASGNLLYIGFRLDGVHCVPTPDSGVVC 407
DB 367 ASVEMSAVA-----PPP-----ASGNLLYIGFRLDGVHCVPTPDSGVVC 407

QY 408 SIFRTDPRFRSVRSTMEDV---GGGLGSHHRELHLILRELQFIFARMKKADEAEELISDW 465
DB 408 G-----RMACSPTHDEHLHGQPPGDPDLAKILEEVRYIANRFRCDSEAVCSEW 460

QY 466 KFAAMVVDRECLFVFTLTIIATVAVLLSAPHII 499
 Db 461 KFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 12

ABG70492
 ID ABG70492 standard; Protein; 502 AA.

XX AC ABG70492;
 XX 06-DEC-2002 (first entry)
 XX DE Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
 XX KW Human; neuronal nicotinic acetylcholine receptor; nAChR; receptor;
 XX KW ion flux; alpha 7 subunit.
 XX OS Homo sapiens.
 XX XX US6440681-B1.
 XX PD 27-AUG-2002.
 XX XX 07-JUN-1995; 95US-0487596.
 XX PR 03-APR-1990; 90US-0504455.
 XX PR 30-NOV-1992; 92US-0938154.
 XX PR 08-MAR-1993; 93US-0028031.
 XX PR 08-NOV-1993; 93US-0149503.
 XX PA (MERI) MERCK & CO INC.
 XX PI Elliott KJ, Ellis SB, Harpold MM;
 XX DR WPI: 2002-711528/77.
 XX DR N-PSDB; ABS54875.

XX PT Identifying antagonists or agonists of human neuronal nicotinic
 PT acetylcholine receptors, by contacting recombinant cells with test
 PT compound, and measuring ion flux of cells or binding of compound to
 PT nAChR
 XX PS Claim 101; Column 59-64; 56pp; English.
 XX CC The invention relates to a method for identifying compounds that are
 CC antagonists or agonists of human neuronal nicotinic acetylcholine
 CC receptors (nAChRs), by contacting recombinant cells with a test
 CC compound and measuring ion flux, the electrophysiological response of the
 CC cells or binding of the test compound to the nAChR. The recombinant
 CC cells are produced by transfection with a nucleic acid encoding at least
 CC one human nAChR (alpha or beta) subunit, such that the cells express an
 CC nAChR comprising one human subunit encoded by the transfected nucleic
 CC acid. This sequence represents the alpha 7 subunit of the human nAChR
 XX polypeptide.

SQ Sequence 502 AA;

Query Match 47.7%; Score 1258.5; DB 23; Length 502;
 Best Local Similarity 48.6%; Pred. NO: 9e-124;
 Matches 250; Conservative 75; Mismatches 138; Indels 51; Gaps 7;

QY 8 LALLA-LLPVSQGPHEKRLNALLANYNTLRLPVRANSEPLEVRFGTLTLOQIIDVDEN 66
 Db 10 LALAALLHVSLLQGEFQRLKLYELKYNPLERPVANDSOPLTVYFSLQLQIMVDEN 69
 QY 67 QLLITNIWLSLEWDYNIWRNDSEYGGVKDLRITPNKWLKPDVLWYNSADEFGDTQYTN 126
 Db 70 QVLTNIWLQMSWTIDHYLQWNVSEYPGVKTRFDPGQIWKPDILLYNSADERFDFATFTN 129
 QY 127 VVVRSGGCLLYPPGIFKSTCKMDIAWPFDDQCHDMKFGSWTYDGNQLDLVKDEAGD 186
 Db 130 VLNVSSGHCQYLPPIGIFKSSCYIDVRWPFDDVQHCKLAFGWSYSGWSDLDQMGE---AD 186

QY 187 LSDFITNGEWLIGMPGKKNITTYACCPYVDVTFIMIRRTLYFFNLIVPCVLSS 246
 Db 187 ISGYIPNGEWDLVIGPKRSERYECCKEPYDPVTFVTRRTLYGLNLLIPCVLISA 246
 QY 247 MALLGFTLPDPGSEKLTGLVTLLSLTVFLNLVAETLPQVSDAIPLLGYFNCIMFWAS 306
 Db 247 LALLVFLLPADSGEKISLGTIVLLSLTVFMLLVAETIMPATSDSVPLIAQYFASTMIIVGL 306
 QY 307 SVVLTVVVNLNYHRTADIHEMPQWIKSVFELQWLPWILRMSRPGCKKITRKTMMNTMREL 366
 Db 307 SVVTVIVLYQYHHDDPGGKMPKWTIVILLNMCWFLMRKPGEDKVRPACQHKQRCSL 366
 QY 367 ELKRSKSLLANVLDDDFRHGPPPPNSTAGNL-----ASGNLLYIGFRLDGVHCVPTPDSGVVC 407
 Db 367 ASVMSAVA-----PPP-----ASGNLLYIGFRLDGVHCVPTPDSGVVC 407
 QY 408 SIFRTDFRRSFVRPSTMEDV--GGGLGSHHRELHLILRELQFITARKKADEAELISDW 465
 Db 408 G-----RMACSPTHDEHLHGPGPEGDPLAKILEEVRYIANFRQDESEAVCSEW 460
 QY 466 KFAAMVVDRECLFVFTLTIIATVAVLLSAPHII 499
 Db 461 KFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 13

AAW69216
 ID AAW69216 standard; Protein; 502 AA.

XX AC AAW69216;
 XX 09-OCT-1998 (first entry)
 XX DE V274T variant human alpha7 nAChR protein.

XX KW Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer;
 KW neurodegeneration; enzyme dysfunction; affective disorder; therapy;
 KW immune dysfunction; diabetic neuropathy; Alzheimer's disease;
 KW schizophrenia.

XX OS Homo sapiens.

XX PN WO9828331-A2.

XX XX 02-JUL-1998.

XX PF 22-DEC-1997; 97WO-US23405.

XX PR 20-DEC-1996; 96US-0771737.

XX PA (ABBO) ABBOTT LAB.

XX PI Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM;

XX PI Roch J, Sullivan JP, Touma E;

XX DR WPI: 1998-377593/32.

XX DR N-PSDB; AAV44687.

XX PT Nucleic acid encoding variant of human alpha7 nicotinic
 PT acetylcholine receptor sub-unit - used to identify modulators of
 PT the receptor, potentially useful for treating neuro-degeneration,
 PT cancer, affective disorders etc.

XX PS Claim 15; Fig 2; 44pp; English.

XX CC This sequence is the V274T variant of human alpha7 nicotinic
 CC acetylcholine receptor (nAChR) subunit of the invention. Cells containing
 CC the DNA are used to express the protein and to identify modulators of
 CC alpha7 nAChR activity or cytoprotective agents, e.g. antisense
 CC compounds or antagonists that are potentially useful for treating
 CC neurodegeneration, enzyme dysfunction, affective disorders and immune
 CC dysfunction, such as cancer, post-herpetic neuralgia, diabetic

CC neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
 CC psychosis and schizophrenia. Probes based on the DNA are used to detect
 CC the DNA in usual hybridisation or amplification tests, while monoclonal
 CC antibodies are used to detect the protein for diagnosis (in vitro or by
 CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 nACHR,
 CC the protein has about 100-fold greater sensitivity to cholinergic
 CC receptor agonists (nicotine or acetylcholine) and response to these
 CC agonists decays more slowly, but the wild-type inward rectification is
 CC retained.

XX SQ Sequence 502 AA;

Query Match 47.5%; Score 1254.5; DB 19; Length 502;
 Best Local Similarity 48.4%; Pred. No. 2.4e-123;
 Matches 249; Conservative 75; Mismatches 139; Indels 51; Gaps 7;

Qy 8 LALLA-LLPVSEQPHKRLNALLANYTLERPVANSEPLEVRFGLTQLQIIDVDEN 66
 Db 10 LALAASLLHVSLOGEFORKLYKELVKNYPLERPVANDSQPLTVYFSLSLQIMDVDEKN 69
 Qy 67 QLLITNIWLSLEWNYLNRWDSYGVKDLRITPNKLNKPDVLMYNSADEGFGDTYQTN 126
 Db 70 QVLTNIWLSQSWTDHYLQWNVSEYPGVKTVPFDDGOIKWPDILLYNSADERFATHTN 129
 Qy 127 VVVRSGSCLYVPGIFKSTCKMDIAWPPDDQCHDKMFGSWTYDGNQLDLVLKDEAGD 186
 Db 130 VLVNSSGHCOYLPPIGIFKSCYIDVRWPFDDVQCHKLKFGSWSYGWSLDLQMOE---AD 186
 Qy 187 LSDFITNGEWYLLMGPKKNTITACCPYVVDVTFIMIRRTLYYFFNLIVPCVLIS 246
 Db 187 ISGYIPNGEWDLVIGPKSRSEFYECCKEPYDVTFVIMRRRTLYYGLNLLIPCVLISA 246
 Qy 247 MALLGFTLPDPSGEKLTGLVILLSLTVFLVAETLPQVSDAIPLLGTYFNCIMFMVAS 306
 Db 247 LALLVFLPADSGEKISIGITVILLSLTFMLVAEIMPATSDSVPLIAQYFASTMIIVGL 306
 Qy 307 SVLTVVVLVNYHHRTADIEHMPQIKSVFLQWLPIWLRMSRPGKTIKTKIMNTRREL 366
 Db 307 SVVTVTVIYQHHDPDGGKMPKTRVILLNWCALFMRKRPGEKDKVRPACQHKRCSL 366
 Qy 367 ELKRSKSLANLALDIDDDFRHGPDPNPNSTAGNL-----GPGC 407
 Db 367 ASVMSAVA-----PPP---ASGNLLYIGFRLDGVHCVPTPDSGVC 407
 Qy 408 SIFRTDFRRSVRSTMEDV---GGGLGSHHRELHLILRELQFITARMKKADEAEELISDW 465
 Db 408 G-----RMACSPTHDEHLLHGOPPEGDPDLAKILEEVRYIANRRCQDESEAVCSEW 460
 Qy 466 KFAAVVDRCFLVFTLTITATVANLLSAPHII 499
 Db 461 KFAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 14

AAW12368
 ID AAW12368 standard; Protein; 502 AA.

XX AC AAW12368;

XX DT 17-JUN-1997 (first entry)

DE Neuron alpha-bungarotoxin binding protein alpha subunit.

XX Neuron alpha-bungarotoxin binding protein alpha 1; cholinergic;
 KW ligand binding; ion channel.

XX Gallus sp.

XX Key Location/Qualifiers
 FH Peptide 1..22
 FT Peptide /label- Sig_peptide
 FT Protein 23..502
 FT /label- Matc_protein

XX US5599709-A.
 PN 04-FEB-1997.
 PD 28-SEP-1989; 89US-0413947.
 PF 28-SEP-1989; 89US-0413947.
 XX 28-SEP-1989; 89US-0413947.
 PR (SALK) SALK INST BIOLOGICAL STUDIES.
 XX Lindstrom JM, Schoepfer RD;
 PI WPI; 1997-118297/11.
 DR N-PSDB; AAT59196.

XX New isolated neuronal alpha-bungarotoxin-binding protein DNA - used
 PT to screen cholinergic agents and other drugs which may affect ligand
 PT binding, ion channel or other activities of the protein.
 XX Example; Fig 2A-B; 18pp; English.

XX The alpha1 subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid
 CC sequences of chick neuronal alpha-bungarotoxin binding protein
 CC (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97)
 CC obtd. from an 18-day chick embryo cDNA library. ABBP subunits can
 CC be produced in recombinant host cells, pref. a bacterium, and used
 CC in the screening of cholinergic agents and other drugs that may
 CC affect the ligand binding, ion channel or other activity of intact
 CC ABBP subtypes. The ABBP alpha1 and alpha2 subunits can also be
 CC used to produce subunit peptides for use as immunogens for
 CC preparing antibodies to permit affinity purification of subtypes
 CC and their histological location.

XX SQ Sequence 502 AA;

Query Match 47.5%; Score 1253; DB 18; Length 502;
 Best Local Similarity 48.8%; Pred. No. 3.5e-123;
 Matches 250; Conservative 81; Mismatches 145; Indels 36; Gaps 8;

Qy 2 APLAALALLALLPVSQGPHEKRLNALLANYTLERPVANSEPLEVRFGLTQLQIID 61
 Db 5 ALMLWLLAAGLVRESLOGEFORKLYKELKNYPLERPVANDSQPLTVYFSLSLQIMD 64
 Qy 62 VDEKQQLITNIWLSLEWNYLNRWDSYGVKDLRITPNKLNKPDVLMYNSADEGFGD 121
 Db 65 VDEKQVLTITNIWLTQWYTDHYLQWNVSEYPGVKNRFPDGLIWKPDILLYNSADERF 124
 Qy 122 TYQTNVVRSGSCLYVPGIFKSTCKMDIAWPPDDQCHDKMFGSWTYDGNQLDLVLK 181
 Db 125 TFFTNVLVNSSGHCOYLPPIGIFKSCYIDVRWPFDDVQCHKLKFGSWSYGWSLDLQMOE 184
 Qy 182 EAGDLSDFITNGEWYLLMGPKKNTITACCPYVVDVTFIMIRRTLYYFFNLIVPC 241
 Db 185 ---ADISGYISNGEWDLVIGPKRSEFYECCKEPYDITFTVIMRRRTLYYGLNLLIPC 241
 Qy 242 VLISSMALLGFTLPDPSGEKLTGLVILLSLTVFLVAETLPQVSDAIPLLGTYFNCIM 301
 Db 242 VLISALALLVFLPADSGEKISIGITVILLSLTVFVLLVAEIMPATSDSVPLIAQYFAST 301
 Qy 302 FMAVSSVVLTVVLYNHHRTADIEHMPQIKSVFLQWLPIWLRMSRPGKTIKTKIMN 361
 Db 302 IIVGLSVVTVTVIYQHHDPDGGKMPKTRVILLNWCALFMRKRPGEKDKVRPACQHK 361
 Qy 362 RMRELELERSKSKS-----LLANVLIDIDDDFR-----HGPPPPNPNSTAGNLGPGCSIFRT 412
 Db 362 RRCSSSEMNTVSGQCSNGLYI--GFGLDGVHCTPTTDSGVICGRM--TCS-----413
 Qy 413 DFRSFRVSRPSTMEDVGGGLGSHH-----RELHLILRELQFITARMKKADEAEELISDW 467
 Db 414 -----PTEENL---LHSGHPSEGDPLAKILEEVRYIANRFRDODEEAICNENK 462
 Qy 468 AAMVVDRCFLVFTLTITATVANLLSAPHII 499

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 21, 2003, 03:48:31 ; Search time 3282.73 Seconds
(without alignments)
11127.831 Million cell updates/sec

Title: US-09-303-232-5_COPY_95_1597

Perfect score: 1503

Sequence: 1 atggccctatgttggcgc.....cacgcgcatcatcgatgcaa 1503

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	423.8	28.2	885	10	BG632919
2	331.2	22.0	607	9	AI292581
3	301.2	20.0	1201	9	AL530299
4	293.2	19.5	2940	11	AK034228

5	293.2	19.5	3230	11	AK083157	Mus muscu
6	281.6	18.7	3483	11	AK081254	Mus muscu
7	281.6	18.7	4037	11	AK049722	Mus muscu
8	281.6	18.7	4046	11	AK051742	Mus muscu
9	275.6	18.3	1864	11	AK053497	Mus muscu
10	275.6	18.3	2316	11	AK051730	Mus muscu
11	275.6	18.3	3126	11	AK080415	Mus muscu
12	258.8	17.2	2010	11	AK080475	Mus muscu
13	256.6	17.1	833	14	CB245337	UI-M-FY0-
14	246.2	16.4	4290	11	AK029177	Mus muscu
15	240	16.0	908	13	BUI49265	AGENCOURT
16	239.2	15.9	922	13	BUI15857	AGENCOURT
17	236.8	15.8	1036	13	BX437801	BX437801
18	234.8	15.6	755	13	B0702422	UI-M-FY0-
19	228.2	15.2	615	14	CB149460	K-EST0205
20	220.4	14.7	2513	11	AK033068	Mus muscu
21	212.6	14.1	1034	13	BX403124	BX403124
22	210.8	14.0	755	10	AK914206	EST345510
23	210.4	14.0	658	12	BW711715	UI-E-CLL-
24	210.4	14.0	797	14	CA326954	UI-M-FY0-
25	202.2	13.5	939	13	B0720344	AGENCOURT
26	202	13.4	607	14	CA751482	UI-M-FY0-
27	201.8	13.4	4589	11	AK030464	Mus muscu
28	199.2	13.3	720	14	CA373069	647093 NC
29	198	13.2	763	14	CA374163	648474 NC
30	194.8	13.0	411	12	BI516733	BB160023A
31	193.8	12.9	410	12	BI516843	BB160023B
32	193.6	12.9	640	14	CB244439	UI-M-FY0-
33	192.8	12.8	2074	11	AK087554	Mus muscu
34	192.2	12.8	932	29	CNS02DCP	Tetraodon
35	190.6	12.7	1001	29	CNS03RTG	Tetraodon
36	188.4	12.5	882	12	BI195149	602944157
37	188.2	12.5	1101	29	CNS000IF	Drosophila
38	187.2	12.5	1007	29	CNS00HJU	Drosophila
39	186.8	12.4	3827	11	AK041217	Mus muscu
40	183.8	12.2	1835	11	AK010496	Mus muscu
41	182.8	12.2	586	13	BX299163	BX299163
42	179.8	12.0	978	29	CNS006F9	Drosophila
43	179.6	11.9	830	10	BG190899	RST9980 A
44	177.8	11.8	809	10	BG404575	602420721
45	176.6	11.7	672	10	BB637693	BB637693

ALIGNMENTS

RESULT 1

BG632919/c

LOCUS

DEFINITION

BG632919 885 bp mRNA linear EST 23-APR-2001
GH16126.3prime GH Drosophila melanogaster head POT2 Drosophila
melanogaster cDNA clone GH16126 3 similar to CG4128: FBan0004128
'ion channel', located on: 2L 30D1-30E1:: 04/10/2001, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Other_ESTs: GH16126.5prime

Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd,

Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Based upon the presence of a XhoI site followed by a run of 14 or

QY 131 AGAGCGAAGCGGTAGAGGTTCGGCTTGACCTTGACGAGAAATCATTTGACGTGGACG 190
D 195 AATCGGAGCCCTGGGAGTTAAGTTCGGACTACGCTGCAGCAGATCATCGACGTGGACG 254
QY 191 AGAAGAAATCAACTACTATATAACCAATATATGCGTGTGCTGGAGTGAATGACTACAACC 250
D 255 AGAAGAAATCAGCTTCTATACCAATATCTTGGCTTTCGGTGGAGTGAACGACTACAATC 314
QY 251 TGAGGTGGACGACGAGTATGCGGGGTCAAGGACCTCAGGATCAGCCCCCAACAAGT 310
D 315 TGGCTGGAAATGAACGGAATACGCGGGGTCAAGGATCTACGAATCAGCCCCCAACAAGC 374
QY 311 TGTGGAGCGGACGCTCTATATATATAGTCTGACGAGGCTTTGGAGGACCTAC 370
D 375 TGTGGAGCGGACGCTCTATATATAGTCTGACGAGGCTTTGGAGGACCTAC 434
QY 371 AGACCAAGCTGTGGTTCAGAGCGGCGGAGTTCCTGTACGTCGACCTGGCATATTC 430
D 435 ACACGAGCTGTGGTTCAGAGCGGCGGAGTTCCTGTACGTCGACCTGGCATATTC 494
QY 431 AGACCAATGCAAGATGACATCGCTGTGCTTCCCTTCGACGACCAACACTGTGATATGA 490
D 495 AGACCAATGCAAGATGACATCGCTGTGCTTCCCTTCGACGACCAACACTGTGATATGA 554
QY 491 AGTTCGCTAGCTGACATGACGCGCAATCAGTTGGATCTGGTGCTAA 538
D 555 AATTCGCTAGTTCGACTTACGATGGAATCAGTTGGATTTGGA 602

RESULT 3

AL530299

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL530299 1201 bp mRNA linear EST 23-MAY-2003
AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.
AL530299
AL530299.2 GI:31068132
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12793792.
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7646.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DD007CH03QPL&cluster=7646.r. Contact :
Feng Liang Email : fliang@life.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DD007CH03QPL.

FEATURES

source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DD007YP05"
/tissue.type="NEUROBLASTOMA COT 50-NORMALIZED"
/clone.lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
258 a 326 c 319 g 273 t 25 others
BASE COUNT
ORIGIN

Query Match 20.0%; Score 301.2; DB 9; Length 1201;
Best Local Similarity 60.2%; Pred. No. 3e-72;
Matches 537; Conservative 10; Mismatches 333; Indels 12; Gaps 3;

QY 65 ACCGAGAGAGACTCCTGAACGCTTCTGCGGCAACTACACACCTTGGAGCGACCGGTGG 124
D 197 WCCAGAGGAGCTTTACAAGGAGCTGGTCAAGAACTACAATCCCTTTGGAGAGCCCGGTGG 256
QY 125 CCAACGAGAGCGAAGCGCTAGAGGTTCAGGTTTCGGCTTTCAGCTTTCGACGAAATCATTTGACG 184
D 257 CCAATGACTCGCAACCACTCACCCTTCTCTCCCTGAGCCCTCTTCGAGATCATCGACG 316
QY 185 TGGACGAGAGAAATCAACTACTTATTAACCAATATATGGTGTGCTTGGTGGAGTGAATGACT 244
D 317 TGGATCAGAAGAACCAAGTTTAAACCAACCAATTTGGCTGCAAAATGTCTTGGACATC 376
QY 245 ACAACCTGAGGTGGAGACGACGAGTATGGCGGGGTCAAGGACCTCAGGATCACGCCCA 304
D 377 ACTATTACAGTGAATGTGTCAAGATATCCAGGGGTGAAGACTGTTCGTTTCCCCAGATG 436
QY 305 ACAAGTTGTGGAAGCGGACGCTCTTATGTATAATAGTCTGACGAGGTTTTCGACGGGA 364
D 437 GCCAGATTTGGAACCAACAGACATCTTCTCTATAACAGTCTGATGAGCGCTTTGACGCCA 496
QY 365 CTTACGACCAACAGTGGTGTGAGAAAGCGGGGAGTTGCCCTGTACGTGCCACCTGGGCA 424
D 497 CATTCACACTAACGTTGTTGGAATTTCTTGGGCAATGGCAATGGGACCTAGTGGGATCC 556
QY 425 TATTCAGACGACATCAAGATGGACATCGCTGGTTCCTTCGACGACCAACACTGTG 484
D 557 TATTCAGAGTTCCTCTACATCGATGATCGCTGGTTCCTTTGATGTGACGACTGCA 616
QY 485 ATATGAAGTTTCGCTAGCTGACATATGACGCGCAATCAGTTGGATCTGCTGCTAAAAGATG 544
D 617 AACTGAAGTTTGGCTCTGCTCTTACGAGGCTGGTCTTGGATCTGCAGATGCAGGA-- 674
QY 545 AGCAGGCGGCGATCTATCGGACTTCATACAAATGGGAGTGGTATCTAATAGGAATGC 604
D 675 -----GGCAGATATCAGTGGCTATATCCCAATGGAGAATGGGACCTAGTGGGATCC 727
QY 605 CAGGCAAAAGAACACAATAACATACGCTGCTGCCCGCCGACCTACGTGGAGTCACT 664
D 728 CCGGCAAGAGGAGTGAAGGTTCTATGAGTCTGCAAGAGCCCTACCCCGATGTCACT 787
QY 665 TCACCATCATGATAAGAAGCAACCTTGTACTTCTTCAACCTGATGCTGCCCTGGG 724
D 788 TCACAGTACCATGCGCCCGCAGGACCTCTACTATGCGCTCAACCTGCTGATCCCTGTG 847
QY 725 TCGTATCATCGATGGACCTCTCGGCTTCACATGCGCAGCACTCGGAG--AGAA 782
D 848 TGTCTATCTCCGCCCTCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907
QY 783 ACTCAGCTTGGAGTCACTATTTCTATCGCTGACGCTGCTTCTCAACCTGCTGCTGCTGCTG 842
D 908 ATTTCCTTGGGATTAACAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 967
QY 843 GACCTCTGCCACAGCTCTCCGAGCTATCCCTCTTGTAGGACGCTACTTCAATTTGATCAT 902
D 968 GATATGCGCCGCAACATCCGATTCGGTACCATTTGAGGCCAGCTTCTTCCGACGACCAT 1027
QY 903 GTTCATGTAGGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 954
D 1028 GATCATCGT-GGGCTTTGGGTGTTGKRMGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1078

RESULT 4

AK034228

LOCUS

DEFINITION

ACCESSION

VERSION

AK034228 2940 bp mRNA linear HTC 05-DEC-2002
Mus musculus adult male diencephalon cDNA, RIKEN full-length
enriched library, clone:933016516 product:cholinergic receptor,
nicotinic, alpha polypeptide 4, full insert sequence.
AK034228
AK034228.1 GI:26329798

QY	251	TGAGGTGGACGACGACGAGTATGCGCGGGTCAAGGACCTCAGGATCAACGCCCAACAAGT	310
Db	414	TGCGCTGGGACCCCTGGTGTACGAGAAATGTCACCTCCATCCGATCCCATCTGAACCTCA	473
QY	311	TGFGGAAGCGGACGCTCTATGTAATAAGTAGCTCAGCAGGGTTTGTGACGGGACTACC	370
Db	474	CTGGAAGGCTGACATGCTCTCAACAACCGGACGGGACTTTGACGATCAACCCACC	533
QY	371	AGACCAAGCTGTGGTTCAGAAGCGGCGGAGTTGCTGTACGTGACCTGGCACCATTATCA	430
Db	534	TAACCAAGCCCACTGTTCTATGATGGCGGTGTCAGTGGACACCCCGGCCATCTATA	593
QY	431	AGAGCACATGCAGATGGACATCGCTGGTGTTCCTTCAGCAGCAACACTGTGATGATGA	490
Db	594	AGAGCTCTTCGACATCGACGTCACCTTCTCCCTTCGACGACGAGAACTGTACCATGA	653
QY	491	AGTTCCGTAGCTGACATATGACGCAATCTAGTTGATCTGTTGCTTAAAGATGAGCGAG	550
Db	654	AGTTTGGGCTGGACCTACGACAGGCCAAGATTGACTTGGTGACATGCACAGCCGTG	713
QY	551	GCGGCGATCTATGGGACTTCAATAAANAATGGGAGTGGTATCTTAATAGGAATGCCAGCA	610
Db	714	TGGACCAACT---GGACTTCTGGGAAAGTGGGAGTGGTCAATTGTTGGATGCGTGGCA	770
QY	611	AAAGAACACATAATACGCTGCTGCCCGAGCCCTACGTGGAGCTCACTTCACCA	670
Db	771	CCTACACACACAGGAATATGATGCTGTCCGAGAGATCTATCTGACATCACTAGCCCT	830
QY	671	TCAATGATAAGACGACCACTTGTACTACTTCTTCAACCTGATCGTCCGCTGGTCTCA	730
Db	831	TCATCATCGCGGACTGCCACTGTTCTACACCATCAACCTTATCATCCCGTCCCTGCTCA	890
QY	731	TCATCATGATGGCACTCTCGGCTTCACACTGCGACAGACTCCGAGAGAACTCACAC	790
Db	891	TCCTCTCCCTCACCGTGGTCTTCTATCTGCGCTCGAGTGGCGGAGAGGTCACGC	950
QY	791	TTGGAGTCACTATTCTTCTATCGCTGACGGTGTCTCAACCTGGTAGCCGAGACCTGC	850
Db	951	TGTGCATCTCGGTCGCTTCTCTCACCGTCTTCTGCTGCTCAATCAACCGAGATCATCC	1010
QY	851	CACAGCTCTCCGACGCTATCCCTCTTAGGAGAGTACTTCAATTCATCTGTTTCATGG	910
Db	1011	CGTCCACCTCGTGGTCACTCCGCTCATCGGAGAGTACTCTTTCACCATGATCTTGG	1070
QY	911	TAGCGTCTGTGTGACTGTTGGTGGTACTCAATTAACCATCGCAACAGCTGATA	970
Db	1071	TCACCTCTCCATGTCATCAGGCTCTTCTGCTCAATGTACACCACTCCACCAAGCA	1130
QY	971	TACATGAATGCCACAGTGGATAAATCAGTATCTTACATGTTGGTGGATGATCTGC	1030
Db	1131	CACACACCATGCGCGCTGGTGGCGAGAGTCTTCTGACATGTTGCCCCCTCTCTCT	1190
QY	1031	GAATGTCGAGGCCA 1044	
Db	1191	TCATGAGCGGCCA 1204	
RESULT 5			
AK083157			
LOCUS			
DEFINITION			
AK083157			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,

Arawaka, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,

Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,

Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,

Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,

Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,

Kuehl, P., Lewis, S., Matsuo, Y., Nikaudo, I., Pesole, G.,

Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,

Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,

Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,

Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,

Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,

Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,

Machinoni, L., Mashima, J., Mazzarelli, J. N., Mombaerts, P., Nordone, P.,

Ring, B., Rinchald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,

Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,

Toyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,

Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsuke, S.

and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660

11217851

5

The FANTOM Consortium and the RIKEN Genome Exploration Research

Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation

of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

6 (bases 1 to 3230)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,

Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,

Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,

Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,

Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,

Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,

Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,

Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,

Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of

Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail: genome-res@cg.riken.go.jp,

URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: <http://genome.gsc.riken.go.jp/>
 URL: <http://fantom.gsc.riken.go.jp/>.

FEATURES

Location/Qualifiers
 1..3230
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 LAGNI"

CDS

BASE COUNT 699 a 992 c 816 g 723 t
 ORIGIN

Query Match 19.5%; Score 293.2; DB 11; Length 3230;
 Best Local Similarity 55.9%; Pred. No. 7.8e-70;
 Matches 578; Conservative 0; Mismatches 453; Indels 3; Gaps 1;

Qy 11 TGGTGGCGGCTTGGCGTGTGCTTGTGCTGCGGATGCGAGCAAGGTCCTCACGAGA 70
 Db 94 TCTTAGGACCGGCTTGTGCTGTAGCAGCCACATAGAGACCGCGGCCCATCGGAGG 153
 Qy 71 AGACACTCTGAACCGTGTGCGGCACTACACACCCCTGGACCGCGGTGCCCAACG 130
 Db 154 AGCGGCTCTGAGAGACTCTTCTCTGGCTACACAAAGTGCTGCGGCGAGTAGCCAA 213
 Qy 131 AGACGCAACCGCTAGAGTCAAGTTCGGCTTGACCTTGCAGCAAAATCATTCAGCTGGAGC 190
 Db 214 TCTCAGATGTGCTTGTGCGCTTGGCTGTGCTGATGCTCAGCTCATTTGATGTGATG 273
 Qy 191 AGAAGATCAACTACTTATACCAATATATATGGCTGTGCTGGTGGAGTGAAGTACTACAA 250
 Db 274 AGAAAAACCATGATGACGACCAACGCTGGTGGTGAAGCAGGAGTGGCATGACTACAAAC 333
 Qy 251 TGAGTGAACGACGAGCTATGCGGGGTCAAGGACCTCAGGATCATCCGCCCAACAGT 310
 Db 334 TGCCTGGGACCGCTTGTGCTGACTACAGAAATGTCACTCATCCGATCCCATCTCAACTCA 393
 Qy 311 TGTGGAAGCCGCGCTCTTATGATATATAGTGTGACGAGGGTGTTCAGCGGACCTACC 370
 Db 394 TCTGGAGCCGTGACATGCTCTCTACACACGCGGAGCGGAGCTTTGCAGTCAACCCACC 453

Qy 371 AGACCAACAGTGGTGGTTCAGAAAGCGGCGAGTTCGCTGTAGTGCCACCTGGGCATATCA 430
 Db 454 TAACCAAAAGCCACCTCTTCTATGATGGCGTGTGCAGTGCACACCCCGCCATCTATA 513
 Qy 431 AGACGACATCAAGATGAGATCCGCTGGTTCCTTCGAGGACCAACACATGTGTATGA 490
 Db 514 AGAGCTCTCGAGCATCGAGTCACTTCTTCCCTTCGACGACGAACATGTACCATGA 573
 Qy 491 AGTTGGTAGTGTGACATATGACGGCAATCAGTTGGATCTGGTCTAAAAGATGAGGAG 550
 Db 574 AGTTGGTCTGACCTAGACACCAAGGCCAAGATGACTGGTGAGCATGCACAGCCGCTG 633
 Qy 551 GCGCGGATATCGGACTTTCATACAAATGGGAGTGGTATCTATATAGGAATGCCAGCA 610
 Db 634 TGGACCAACT--GGACTTCTGGAAAGTGGGAGTGGTCTATGTGTGATGCTGCCGCA 690
 Qy 611 AAAAGACACAATAACATACGCGTGTGCCCCGAGCCCTACGTTGGAGCTCACCTTCAACA 670
 Db 691 CCTACAACACCAAGGAAGTAAATGCTGTCGCGAGATCTATCTTGACATCACCTTACGC 750
 Qy 671 TCATGATAAGAAAGACGAACCTTGTACTACTTCTTCAACCTGATCGTCCCGTGGCTGTA 730
 Db 751 TCATATCCCGGACTGCCACTGTCTACACCATCAACCTATATCATCCCGTGGCTGCTCA 810
 Qy 731 TCTCATGATGGGACTCTCTCGGTTACACTGCCACGAGCTCGGAGAGAACTACAC 790
 Db 811 TCTCTCGCTCACCGTGTGTCTTCTATCTGCTGCTGCGGAGTGGCGGAGAGGTACCG 870
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 Qy 851 CACAGGCTCTCGGACCTATCCCCCTGTAGGAGCTACTTCAATTCATGCTCATGTTCATGG 910
 Db 931 CGTCCACCTCGTGTGCTATCCCGCTCATCGCGAGTACCTGCTTCCACCATGATCTCG 990
 Qy 911 TAGCGTCTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 970
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 Db 1051 CACACCATGCGCGCTGGTGGCGAGAGTCTTCTCTGGACATGTGCTGCTGCTGCTGCTGCT 1110
 Qy 1031 GAATGTCGAGGCCA 1044
 Db 1111 TCATGAAGCGCCCA 1124

RESULT 6
 AK081254
 LOCUS
 DEFINITION
 AK081254 3483 bp mRNA linear HTC 05-DEC-2002
 Mus musculus adult male corpus striatum cDNA, RIKEN full-length
 enriched library, clone: C030030P04 product: cholinergic receptor,
 nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
 AK081254
 VERSION
 AK081254.1 GI:26099790
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Mus musculus
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1
 REFERENCE
 AUTHORS
 Carninci, P. and Hayashizaki, Y.
 TITLE
 High-efficiency full-length cDNA cloning
 JOURNAL
 Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE
 99279253
 PUBMED
 10349636
 2
 REFERENCE
 AUTHORS
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

3
STAT

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. KIKEN integrated sequence analysis (RISA) system - 394-format

TITLE

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

sequencing pipeline with 384 multiplexed
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

1000/01T

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Arakawa, T., Hara, A., Nishikishi, Y., Konno, H., Adachi, J., Fukuda, S.,
Aizawa, K., Izawa, M., Fukuji, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
Saito, T., Okazaki, Y., Goshobori, T., Bono, H., Kasukabe, T., Saito, R.,
Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T.,
Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H.,
Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G.,
Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M.,
Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H.,
Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,
Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
Mazzionni, L., Mashima, J., Mazzarelli, J. H., Mombaerts, P.,
Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H.,
Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H.,
Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L.,
Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S.

TTTTT

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

Functional annotation of a full-length
cDNA from *Mytilus* sp. (GenBank accession
number: F04821), 685-690 (2001)
21085660
11217851

5
TCN/TTT

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3483)

Adachi, J., Aizawa, K., Akimura, T., Arikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saotome, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

ENTER

TITLE
JOURNAL

Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

CONVENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.

Query Match		18.7%	Score 281.6;	DB 11;	Length 4037;
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Qy	159	CTTGACCTTCGACGAATCATTTGACGTGGACGAGGAAGTCAACTACTTTATAACCAATAT	218		
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Qy	459	GTTTCCCTTCGACGACCAACACTGTGATATGAAGTTTCGGTGTGACATATCACGGCAA	518		
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Qy	579	TGGGGAGTGTATCTAATAGGAATGCCAGGCAAAAGAACACATAACATACCGTGTCTG	638		
Db	799	TGGGGAGTGGGACATATCGCATGTCCAGGCCCGACGCAAGCAACCGACACCTCC--	856		
Qy	639	CCCGAGCCCTAGCTGGACGTCACTTTCACCATCATGATAGAAGACGAACCTTGTACTA	698		
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RESULT 8

AK051742

LOCUS

AK051742

4046 bp

mRNA

linear

HTC 05-DEC-2002

RESULT 8
AK051742
LOCUS

DEFINITION	Mus musculus 12 days' embryo spinal ganglion cDNA, RIKEN full-length enriched library, clone:PI30070121 product:cholinergic receptor, nicotinic, beta polypeptide 2 (neuronal), full insert sequence.
ACCESSION	AK051742
VERSION	AK051742.1 GI:26342173
KEYWORDS	HTC; CAP trapper.
SOURCE	Mus musculus
ORGANISM	Mus musculus (house mouse)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	20499374
PUBMED	11042159
REFERENCE	3
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakauchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staab, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, F., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21083660
PUBMED	11217851
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 4046)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Koima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES

Location/Qualifiers

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BASE COUNT 878 a 1127 c 1077 g 964 t

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Query Match 18.7%; Score 281.6; DB 11; Length 4046;

Best Local Similarity 57.7%; Pred. No. 1.4e-66;

Matches 547; Conservative 0; Mismatches 389; Indels 12; Gaps 2;

QY 99 CTACAAACACCTGTGAGGACCGGTGGCGCAAGCAGAGCGGACCGCTAGAGGTTCAGGTCGG 158

DB 331 CTATACACAGCTGATCCGTCAGCTACTATGCTCTGAGCTGGTACTGATACAGCTCAT 390

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RESULT 9
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LOCUS
DEFINITION
AK053497
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:El30103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE

AK053497 1864 bp mRNA linear HTC 05-DEC-2002
Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:El30103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.
AK053497
AK053497.1 GI:26343494
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to


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BASE COUNT 735 a 756 c 656 g 769 t
ORIGIN

Query Match      18.3%; Score 275.6; DB 11; Length 2916;
Best Local Similarity 54.7%; Pred. No. 5.8e-65;
Matches 570; Conservative 0; Mismatches 469; Indels 3; Gaps 1;

Qy  3  GGCCCTATCTTGGCGCCTTGGCGCTGCTGGCTTCTGCTGCCGTATCGGAGCAAGGTCC 62
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Qy  63  TCACGAGAAGAGACTCCTGAACGGTGTCTGGCGGAACACAAACCCCTGGAGCGACCGGT 122
Db 250 AGCTGAGCACCCTGTTCCAGTACCTTGTTGAAGATTACAACGAGATCATCGGCCGT 309

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Qy 363  GACCTACCACCAACGCTGGTGGTCAGAACGGCGGCGAGTTGCTGTACGTGCCACCTGG 422
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Qy 483  TGATATGAAGTTCGGTAGTGGACATATGACGCAATCAGTTGGATTCGTGCTGCTAAAGA 542
Db 670 CACCATGAAGTTCGGCTCCTGGTCCCTACGACAAGGCAAGATGACGCTGCTCTCA --T 726

Qy 543  TGAGGACGGCGGATCTATCGGACTTCATAACAATATGGGAGTGGTATCTAATAGGAAT 602
Db 727 TGCTCTCTCAAGACCTCAAGGACTATTGGGAAAGTGGGAGTGGGCCATCATTTAAGC 786

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Qy	603	GCACGGGAAAAGAACACAAATACATACGCGGTGCTGCGCCGAGCCCTACGTGACGCTCAC	662
Db	787	CCCGGGCTCAAAACATGAATCAAGTACAACTGCTGTGAGGAGATCATCCCAAGACATCAC	846
Qy	663	CTTCACCATCATATAGAAGACGAACCTTGTATCTACTTCTTCAACCTGATCGTCCCGTG	722
Db	847	GTACTCGCTATACATTCGCGCGCCTGCGGCTGTCTACACCATCAACCTCATCATTCGCTG	906
Qy	723	CGTGTCTGATCTCATGATGGCACTCCTCGGCTTTCACACTGCCACAGACTCCGGAGAGAA	782
Db	907	CCTGCTCATCTCCTCTACTGCTGCTGCTTCTACTCTGCCCTCGGACTGTGGGAGAA	966
Qy	783	ACTTCACACITGGAGTACATATCTTCTATCGCTGCAGGGTGTTCCTCAACCTGCTGACCGA	842
Db	967	GGTGAGCGCTCGATCTCCGCTGCTCTCTCCCTGACGGGTCTTCTCTCTCGTGATCACCGA	1026
Qy	843	GACCTCGCCACAGGCTCTCCGACGCTATCCGCCCTGTTAGGACGCTACTTCAATTCGATCAT	902
Db	1027	GACCATCCCTTCCACCTCACTGCTGCTATCCCTTGTATCGGGGAGTACCTCTCTCACTAT	1086
Qy	903	GTTTCATGTTAGCGTCTGCTGTTGTTACTGACTGTGGTGGTACTCAATTTACCAACATCGAAC	962
Db	1087	GATTTTGTCACTTGTCCATCTGCTCATCAAGCTCTTGTGCTCAACGTGCACACAGAAC	1146
Qy	963	AGCTGATATATGAATGAATGCCACAGTGGATATAAATCAGTATTCCTCAAAATGGTTCGCATG	1022
Db	1147	TCCGACACACACACAGATGCCACTTGGGTCAAGGCTGTGTTTTGAACCTCTCTCCCAG	1206
Qy	1023	GATACTCGGAATGTCGAGGCCA	1044
Db	1207	GGTTCATGTTTATGACTAGGCCA	1228
RESULT 11			
AK080415			
LOCUS			
DEFINITION			
ACCESSION	AK080415	3126 bp	mRNA
VERSION	AK080415.1	GI:26348538	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Carninci,P. and Hayashizaki,Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE			
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kusunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaquchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,K., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.		
TITLE	RKEN integrated sequence analysis (RISA) system--394-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	20530913		

QY	723	CGTGGCTCATCTCATGATGCCACTCCTCGGCCTTCACACTCCGACCAGACTCCGGAGAA	782
Db	904	CCTGGCTCATCTCCTCTCACTGTGCTGCTTTCTATTCTGCCCCCTCGGACTGTGGGAGAA	963
QY	783	ACTCACACTTGGAGTGACTTAATCTTCTATCGCTGACGGTGTTCTCCTCAACCTGTGACCGA	842
Db	964	GGTGACGCTCTGCATCTCCGTCTCTCTCCCTGACGGTCTTTCTCTCTGTGATCACCGA	1023
QY	843	GACCCCTGCCACAGGTCTCCGACGCTATCCCCTGTTTAGGGACGTACTTCAAAATGCATCAT	902
Db	1024	GACCATCCCTTCCACCTCACTGTGCTATCCCTTGATCGGGGAGTACCTCCTCTTCACTAT	1083
QY	903	GTTTCATGGTAGCTGCTGTGTGACTGACTGTGGTGTTACTCAATACCAACATCGAAC	962
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QY	963	AGCTGATATACGAATGACAGTCCACAGTGGATAAAATCAGTATTCTACAATGGTTGCCATG	1022
Db	1144	TCCGACCACACACAGATGCCCACTGGGTCAAGGCTGTGTTTGAACCTTCTCCCCAG	1203
QY	1023	GATACTGCGAATGTCGAGGCCA	1044
Db	1204	GGTGATGTTTATGACTAGGCCA	1225
RESULT 12			
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LOCUS		2010 bp mRNA linear HTC 05-DEC-2002	
DEFINITION		Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730038F1 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.	
ACCESSION		AK080475	
VERSION		AK080475.1 GI:26099260	
KEYWORDS		HTC; CAP trapper.	
SOURCE		Mus musculus (house mouse)	
ORGANISM		Mus musculus	
REFERENCE		Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;	
AUTHORS		1 Carninci,P. and Hayashizaki,Y.	
TITLE		High-efficiency full-length cDNA cloning	
JOURNAL		Meth. Enzymol. 303, 19-44 (1999)	
MEDLINE		99279253	
PUBMED		10349636	
REFERENCE		2	
AUTHORS		Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.	
TITLE		Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	
JOURNAL		Genome Res. 10 (10), 1617-1630 (2000)	
MEDLINE		20499374	
PUBMED		11042159	
REFERENCE		3	
AUTHORS		Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Sami.N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,I., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.	
TITLE		RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer	
JOURNAL		Genome Res. 10 (11), 1757-1771 (2000)	
MEDLINE		20530913	
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REFERENCE		4	
AUTHORS		Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Akizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondou,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,	

Db 181 ATCCCATCTGAACATCATCTGGAGGCGCTGACATCGCTCTCTACAACAACCGGACGGGAC 240
 QY 335 TTTCAGGAGACCTACCAGCAACACCTGGTGTGTCAGAGCGGCGGAGTTCCTGTACGTG 414
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RESULT 14
 AK029177
 LOCUS
 DEFINITION
 Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4831406G09 product:cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle), full insert sequence.
 AK029177
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 PUBMED
 10349636
 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
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 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanaka, I., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, A., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
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 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yananaka, I., Saito, T., Okazaki, Y., Gojohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Giusti, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nakado, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Mombauts, P., Nordone, P., Ring, B., Rongwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 21085660
 MEDLINE
 11217651
 5
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)
 6 (bases 1 to 4290)
 Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
 Direct Submission
 Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.go.jp/
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Best Local Similarity 54.6%; Pred. No. 1e-56;

Matches 535; Conservative 0; Mismatches 438; Indels 6; Gaps 2;

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Db	87	CATGAGACGGCTGTGGTGGCAAGCTCTTTGAAGACTACAGACTAGTGTCCGGCCAGT	146
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Db	147	GAGACACCGGTGAGATGTACAGTACCGTGGCTGTACAGCTGATCCAGCTATATCAAT	206
Qy	184	GTGACAGAGAGAAATCAACTACTTATTAACCAATATATGCTGTGCTGGAGTGAATGAC	243
Db	207	GTGGATGAAGTAATCATGATGTGTGACACCAATGTACGTCTGAAACAGCAATGGGTGAT	266
Qy	244	TACAACTGAGGTGGAACGAGCAGGAGTGTGGGGGTCAAGGACCTCAGGATCACGCC	303
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Qy	304	AACAAAGTTGTGGAAGCCGCGCTCTTATGTATATAGTGTGACGAGGTTTTTGACGGG	363
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Qy	484	GATATGAAGTTGCGTAGCTGACATATGACGGCAATCAGTTGGATCTGGTCTAAAGAT	543
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Qy	781	AAACTCACACTTGGAGTCACTATTCTTCTATCTGCTGACGGTGTTCCTCAACCTGGTAGCC	840
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Qy	841	GAGACCGTGCACAGGTCTCCGAGCTATCCCGCTGTAGGAGCGTACTTCAATTTGATC	900
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RESULT 15

BU149265

LOCUS

DEFINITION

AGENCY: 8443358 Lupski_sympathetic_trunk Homo sapiens cDNA clone

IMAGE: 6192234 5', mRNA sequence.

BU149265

VERSION

KEYWORDS

EST.

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 908)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

cDNA Library Preparation: Life Technologies, Inc.

DNA sequencing by: The I.M.A.G.E. Consortium (LLNL)

Cloning distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LUAM13593 row: 0 column: 19

High quality sequence stop: 598.

Location/Qualifiers

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Not; site_2: SalI; cDNA made by oligo-dT priming.

Directionally cloned using the following adaptors:

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5'-GACTAGTCTTAGATCCGAGCGGCCCGCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life

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ORIGIN					
Query Match	16.0%;	Score 240;	DB 13;	Length 908;	
Best Local Similarity	60.4%;	Pred. No. 2.7e-55;			
Matches 435; Conservative	0;	Mismatches 275;	Indels 10;	Gaps 2;	
QY	33	GGCTTTGGTCCCGTATCGGAGCAAGGTCTCACGAGAGAGACTCCTCGAAGCGTGTGCT	92		
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QY	93	GGGAACTACACACCTCGAGGACCGGTGGCCACAGAGAGCGGTAGAGCTCAG	152		
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Db	231	CTTCTCCCTGAGCTCCTCGCATCATGACGTGGATGAGAGAACAAGTTTTTAACCA	290		
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QY	273	TGGCGGGTCAAGGACCTCAGGATACGCCCCAACAAAGTTGTGGAAAGCGGACGTCCTTAT	332		
Db	351	TCCAGGGTGAAGACTGTTCTGTTTCCAGATGCCAGATTTGGAACACAGACATTTCTTCT	410		
QY	333	GTATATATGCTGACGAGGGTTTTGACGGGACCTACCAGACCACAGTGGTGGTCAGAAG	392		
Db	411	CTATAACAGTGTGATGAGCGCTTTGACGCCACATTTCCACACTTAAGCTGTGGTGAATTC	470		
QY	393	CGGCGGCAGTTGCCTCTAGCTGCCACTGGCATATTTCAAGAGCACATGCAAGATGGACAT	452		
Db	471	TTCTGGGCATTTGCCAGTACTGCCTCCAGCATATTTCAAGAGTTCCTGCTACATCATGT	530		
QY	453	CGCGTGGTTTCCCTTCGACGACCAACACHTGTGATATGAAGTTCGGTAGCTGCACATATGA	512		
Db	531	ACGCTGGTTTCCCTTTGATGTGCAGCACTGCAAACTGAAGTTTGGGTCTCTGGTCTTACGG	590		
QY	513	CGGCAATCATGTTGGATCTGGTCTAAAAGATGAGGAGCGGGCGGATCTATCGGACATTCAT	572		
Db	591	AGGCTGGTCTTTGGATCTGCAGATGCAGGA-----GGCAGATATCAGTGGCTATAT	641		
QY	573	AACAAATGGGAGTGTATCTAATAGGAATGCCAGGCAAAAAGAACACATAACATACGC	632		
Db	642	CCCCAATGAGAAATGGGACCTATGTGGGAATCCCGGCAAGAGGAGTGAAGGTTCTATGA	701		
QY	633	GTGCTGCCCGAGCCCTAGCTGGACGCTCACTTTCAACCATCATGA-TAAGAAGACGAACT	691		
Db	702	GTGCTGCAAAAGACCCCTACCCGATGTCACCTTCAGTCAACCATTTGCCCGCAAGACAC	761		
QY	692	TGTACTACTTCTTCAACCTGATCGTCCCGTGGTGTGATCTCATCGATGGCACTCCTCG	751		
Db	762	TCCTATATGGCTCAACCTGCTGGATCCCGGTGGGGCTCATCTCGCCCTCGCCCTCG	821		

Search completed: August 21, 2003, 13:12:45
Job time : 3285.73 secs

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Db 815 TGGGTGCTGATCTCATCGATGGCACTCCTCGGCTTCACACTGCCACCAGACTCCGGAGAG 874

PD 27-SEP-2001.

PD 27-SEP-2001.

XX 17-FEB-2000 (first entry)
 XX DE H. virescens acetyl-choline receptor DNA from clone Hva7-1.
 XX KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 XX KW neurotransmission; plant protection agent; conductance; ACHR; ds.
 XX OS Heliothis virescens.
 XX PH Key Location/Qualifiers
 XX CDS 335..1825
 XX FT /*tag= a
 XX FT /product= "acetyl-choline receptor"
 XX PN DEL19819829-AL.
 XX PD 11-NOV-1999.
 XX PF 04-MAY-1998; 98DE-1019829.
 XX PR 04-MAY-1998; 98DE-1019829.
 XX PA (PARB) BAYER AG.
 XX PI Adamczewski M, Oellers N, Schulte T;
 XX DR P-PSDB: AAY50815.
 XX WPI: 2000-014207/02.
 XX PT New nucleic acid encoding a nicotinic acetylcholine receptor from
 XX PT insects, used to identify potential insecticides -
 XX PS Claim 1a; Page 14-17; 26pp; German.
 XX CC This invention describes a novel nucleic acid (NA) encoding a nicotinic
 XX CC acetyl-choline receptor (I) from insects which can be used as an
 XX CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 XX CC (also vectors containing it, its regulatory regions, and antibodies
 XX CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 XX CC protection agents that alter conductance of ACHR, potentially useful as
 XX CC insecticides; or (b) genes which encode polypeptides that are involved in
 XX CC formation of functionally related ACHR in insects. (I) are also used to
 XX CC isolate and characterize the specified regulatory regions and for
 XX CC recombinant production of (II). This sequence encodes an acetyl-choline
 XX CC receptor isolated from *Heliothis virescens*.
 XX SQ Sequence 3700 BP; 893 A; 953 C; 944 G; 910 T; 0 other;
 Query Match 38.38; Score 575; DB 21; Length 3700;
 Best Local Similarity 64.6%; Pred. No. 1.9e-150;
 Matches 929; Conservative 0; Mismatches 460; Indels 48; Gaps 3;
 QY 64 CACGAGAAGAGACTCCCTGAACCGCTTCTGGCGAATACAAACCCCTGGAGCGACCGGTG 123
 DB 431 CACGAGAAGCGGTACTGCAACCACTATTGACCACTACACAGTACTGGAGAGCGCCGTC 490
 QY 124 GCCAACGAGAGCGAAGCGGTAGAGTCAGGTTCGGCTTGACCTTGCAGCAAAATCATTTGAC 183
 DB 491 GTCAACGAGAGCGACCGCGCTGCACCTCTCCTTCGGCTCAGCTTCAGATCATCGAC 550
 QY 184 GTGACGAGAGAATCACTACTTATTAACCAATATATGGCTGTGCTGGAGTGAATGAC 243
 DB 551 GTGACGAGAGAAGACCAAGCTTTTAAACAAACATCTGGCTTAAACATAGAGTGAATGAT 610
 QY 244 TACAACTGAGTGGAGACGAGATGTCGGCGGTCAAGGACCTCAGATCAGCGCC 303
 DB 611 ATGAAGTTGAGTGGAGACACTTCAAGTTTCGGCGGGGTCAAGATTTAAGAGTCCCAACC 670
 QY 304 AACAAAGTTGTGAAGCGGAGCGTCTTATGATTAATAGTGTGACGAGGGTTTTGACGGG 363
 DB 671 CACAGACTATGGAACCAAGAGCTCTTATGTATACAAACGCGGAGGAGGTTGACAGC 730

QY 364 ACCTACAGACACACGCTGGTGGTGCAGAACGCGCGCAGTTCCTGTAGCTGCCACCTGGC 423
 DB 731 ACCTATCAACGAACTGGTGGTGCAGAACGCGCTCGTGTGTAGCTGCCCGCCGCGC 790
 QY 424 ATATTCAAGAGCACATCAAGATGACATCGCGTGGTTTCCCTTCGACGACCAACACTGT 483
 DB 791 ATCTTCAAGAGCACCTCAAGATGACATCACCTGGTTCCCTTCGACGACCAACAGATG 850
 QY 484 GATATGAAGTTCGGTAGCTGGACATATGACGGCAATCAGTTGGATCTGGTCTAAAGAT 543
 DB 851 GAGATGAAGTTTGGCAGCTGACATATGATGGTTATCAGTTGGATCTACAACTACAGAT 910
 QY 544 GAGCAGCGCGGCGATCTATCGGACTTCATACAAATGGGAGTGGTATCTAATAGGATG 603
 DB 911 GAAGGGGGCGGAGATATAAGCAGTTTGTACGAATGCGAATGGGAGTTAATAGGATG 970
 QY 604 CCAGGCAAAAAGAACACAATAACATACGCGTGTGCCCGAGCGCTACGTGAGCTCAC 663
 DB 971 CCGGCAAGCGCAACGAGATCTACTACAATGTTGTCGGAGCCATACATGACATCAG 1030
 QY 664 TTCACCATCATGATAAGAGACGAACTTGTACTACTTCTTCAACCTGATCGTCCGPGC 723
 DB 1031 TTTGCGGTGGTATCCGAGGAAACGCTCTACTACTTCTTCAATCTGATGTCGCTGCG 1090
 QY 724 GTGCTGATCTCATGATGCGACCTCTCGGCTTACACTGCCACGAGACTCCGGAGAGAA 783
 DB 1091 GTGCTCATCGCTCCATGGCTTATGGGGTTCACCTTGGCTCCAGACTCCGCGAAGAA 1150
 QY 784 CTCACACTTGGAGTCACTATTCTTATCGGTGACGCTGTTCCTCAACCTGATGCCGAG 843
 DB 1151 TTGCTTTAGTGTGACGATATTAATGCTGTGACGCTGTTCCTCAACATGTTGGCGAG 1210
 QY 844 ACCCTGCCACAGCTCTCCGACGCTATCCCTGTTAGGAGCTACTTCAATTTGATCATG 903
 DB 1211 ACGATGCCAGCGACGTCGCGCGCTGCTTGTGCGCACTACTTCAACTGATCATG 1270
 QY 904 TTCATGTAGGCTGCTGTGGTACTGACTGTGGTGTGCTACTCAATTACCACCATCGACA 963
 DB 1271 TTCATGTGGCTTCCCTCGCTCTCCACCATATGATFCTTCACTACCAACCGGCGAC 1330
 QY 964 GCTGATATACATGAATGCCACAGTGGATAAATCAGTATTTCCTACAAATGGTTGCCATG 1023
 DB 1331 GCACACTCACGAATAGTGAATGATGCTGTTGCGGTGTTCTTTATTGGCTCCGCTGG 1390
 QY 1024 ATACTGGAATGTGAGCGCAGGGAAGAATACACAGGAAGACTATAATGATGAACACG 1093
 DB 1391 GTGCTGCGCATGTACGCGCGCGCTCGCGG---ACGACGCGCGCGCGCGCGCTACCT 1447
 QY 1084 AGGATGAGGAGCTGGAACCTGAAGGAGAGGTGCTGGAAGTCTTGTGGCGCAATGTTCTA 1143
 DB 1448 CCGCGCGGACCTGGAGCTGCGGAGCGCTCTCCAAAGTCTGCTTACGCAAGCTGCTC 1507
 QY 1144 GATATTGATGATGATTCAGACACGCGCTCCGCTCTCTAAACAGTACTGCTCGACCGGG 1203
 DB 1508 GACATCATGACGACTTCCGCCACCCGCAAGCGCAGCAG-----CGCAATGCTGCG 1560
 QY 1204 AATTGGGACCTGGGTGCTCAATATCCGACAGGATTTCCGTCGGTCTGCTCGCTCGCG 1263
 DB 1561 ATACTACAGGGGGGTGAGGAGAATGCGCGGGGTGGCGGCGCAGACTTGTCTTCG---- 1616
 QY 1264 TCCACGATGGAAGAGCTGGGCGGGGCTGGGTAGCCACCATCGGAGCTCAGCTCATATA 1323
 DB 1617 -----GTGTCGACTAGGAGCTCTCCCTCAT 1642
 QY 1324 CTGAGAGAGCTGCACTTATCAGCGCCAGGATGAAGAGGCTGATGAGGAAGCGGAGCTG 1383
 DB 1643 CTGAGAGATAGAGTATCATCAGATCAGATGCGAAGGACGACGAGATGCGACATT 1702
 QY 1384 ATCAGCAGCTGAAGATTTGCTGCGATGTTGTTGATAGGTTTTGCCCTGCTGTTTACA 1443
 DB 1703 TCGCGCGAGTGAAGTTCGCGCGCATGCTGTCGACAGACTGTGCTCTATTATCTTTACC 1762
 QY 1444 CTTTTCACATCATCGCGACAGTAGTCTCTCTGTTATCGGCAACCGCATATCATCGTG 1500

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Db      1763 CTGTTCAATATCGCCACCGTAGCGTGTCTCGCGCCACACATCATGTG 1819
      || ||||| ||||| || ||||| || ||||| || ||||| || ||||| ||
RESULT 4
ABLI13733
XX      ID ABLI13733 standard; cDNA; 936 BP.
XX      AC ABLI13733;
XX      DT 26-MAR-2002 (first entry)
XX      DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 35681.
XX      KW Drosophila; developmental biology; cell signalling; insecticide;
XX      KW pharmaceutical; gene; ss.
XX      OS Drosophila melanogaster.
XX      PN WO200171042-A2.
XX      PD 27-SEP-2001.
XX      PF 23-MAR-2001; 2001WO-US09231.
XX      PR 23-MAR-2000; 2000US-191637P.
XX      PR 11-JUL-2000; 2000US-0614150.
XX      PA (PEXE ) PE CORP NY.
XX      PI Venter JC, Adams M, Li PWD, Myers EW;
XX      DR WPI; 2001-656860/75.
XX      DR P-PSDB; ABB69630.
XX      PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX      PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX      PT interactions -
XX      PS Claim 1; SEQ ID NO 35681; 21pp + Sequence Listing; English.
XX      CC The invention relates to an isolated nucleic acid detection reagent
XX      CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX      CC useful in developmental biology and in elucidating cell signalling and
XX      CC cell-cell interactions in higher eukaryotes for the development of
XX      CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX      CC discloses genomic DNA sequences (ABLI16176-ABLI30511), expressed DNA
XX      CC sequences (ABLI01840-ABLI16175) and the encoded proteins
XX      CC (ABB57737-ABB72072).
XX      CC The sequence data for this patent did not form part of the printed
XX      CC specification, but was obtained in electronic format directly from WIPO
XX      CC at ftp.wipo.int/pub/published_pct_sequences.
XX      SQ Sequence 936 BP; 238 A; 213 C; 239 G; 246 T; 0 other;

Query Match      28.6%; Score 430.6; DB 23; Length 936;
Best Local Similarity 68.5%; Pred. NO. 3.1e-110;
Matches 595; Conservative 0; Mismatches 274; Indels 0; Gaps 0;

QY      19 GCCTTGGCGCTGCTGGCTTTGCTGCCCCGTATCGGAGCAAGGTCTCAGAGAAGAGACTC 78
Db      67 GGCCTGGGACTTTTAAATATGATACCGCTTGTGCGGCTGGAGCCCATGAGAAGCGGCTA 126
QY      79 CTGAACGGCTGCTGGCGAACTACAAACCTCGGAGCGACCGGTGGCCCAAGAGAGCGAA 138
Db      127 CTCACGCCCTCTCGACAACTACAAACCTCGGAGCGCTCGGTGGTCAATGAATCCCAT 186
QY      139 CGCTAGAGGTGAGGTTCCGGCTTGACCTTGCAGCAAAATCAATGACGTGGAGCAGAGAAT 198
Db      187 CCATTGCAACTGAGCTTCGGACTACACTCATCATGAGATATCATGATGTGAGCAAGAAAT 246
QY      199 CAACTACTTAAACCAATATATGCTGTGCTGTGGAGTGGATGACTACAACTGAGGTGG 258
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||

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PR 04-MAY-1998; 98DE-1019829.
XX (FARB) BAYER AG.
XX Adamczewski M, Oellers N, Schulte T;
XX WPI; 2000-014207/02.
DR P-PSDB; AAY50814.
XX
PT New nucleic acid encoding a nicotinic acetylcholine receptor from
PT insects, used to identify potential insecticides
XX
PS Claim 1a; Page 8-12; 26pp; German.
XX
XX This invention describes a novel nucleic acid (NA) encoding a nicotinic
CC acetyl-choline receptor (I) from insects which can be used as an
CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
CC (also vectors containing it, its regulatory regions, and antibodies
CC directed against (I)-encoded proteins) are used to screen for: (a) plant
CC protection agents that alter conductance of AChR, potentially useful as
CC insecticides, or (b) genes which encode polypeptides that are involved in
CC formation of functionally related AChR in insects. (I) are also used to
CC isolate and characterize the specified regulatory regions and for
CC recombinant production of (II). This sequence encodes an acetyl-choline
CC receptor isolated from *Drosophila melanogaster*.
XX
SQ Sequence 2886 BP; 942 A; 687 C; 640 G; 617 T; 0 other;
Query Match 27.4%; Score 411.4; DB 21; Length 2886;
Best Local Similarity 68.8%; Pred. No. 1.3e-104;
Matches 565; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
QY 57 AGGTCTCCACGAGAGAGACTCTCTGAACCGCTTCTGCGCAACTACACACCTCTGGAGCG 116
DB 1295 AGGATATCATCAAAAGAGACTGTACACGATCTTTTGGATCTTATAATACACTAGAACG 1354
QY 117 ACCGGTGGCCAAACGAGCGGACCGCTAGAGGTGAGGTTCGGCTTGACCTGACGAAAT 176
DB 1355 TCCCGTTCTCAATGAATCGGACCGCTTACAAATTAAGCTTTGGTTTAACTTTAATGCAAT 1414
QY 177 CATTTGACGTGACGAGAGAAATCAACTACTTATACCAATATATGGCTGCTGGTAGTG 236
DB 1415 TATCGATGTGACGAGAAATCAATTCGTAGTCACTAATGTGGTTAAACTGGAGTG 1474
QY 237 GAATGACTACAACTGAGTGGACGACGAGGATGATGGCGGCTCAAGACCTCAGAT 296
DB 1475 GAACGACATGAATCTCCGCTTGAACACACCTCCGACTATGCGGAGTAAAGATCTGCGAAT 1534
QY 297 CACGCCCAACAAGTTGTGGAAGCCGAGCTCTTATGATATAATAGTGTGACGAGGTTT 356
DB 1535 ACCGCGGATCGCATCTGGAAGCCGAGCTGCTGATGTACAACTGCGGATGAGGAT 1594
QY 357 TGACGGGACCTACCAACGACGAGTGGTGTGAGAGCGGCGGAGTTCCTGTACGTGCC 416
DB 1595 TGACGGGACCTACCAACGAGAGTGGTGTGCGGACAAACGCTCGTCTATACGTTC 1654
QY 417 ACCTGGCATATTAAGAGACACATGCAAGATGACATCGCTGGTTCCTTCGACGACCA 476
DB 1655 GCGGGGATCTTCAAGTCGAGTGCAGATGCAAGATGACATCAGTGGTTCCTTCGATGACCA 1714
QY 477 ACATGTGATATGAAGTTTCGTAGCTGACATATGACGCAATCAGTTGGATCGGTGCT 536
DB 1715 GCGGTGCGAGATGAAGTTTCGCGAGTTCGACCTACGAGGATTCAGCTGGATTTACAAT 1774
QY 537 AAAAGATGAGGCGGCGGATCTATCGGACTTCATACAAATGGGAGTGGTATCTAAT 596
DB 1775 ACAGATGAACACTGCGGTGATATCAGCAGTTACGTCTCAACGCGGAGTGGGAATCT 1834
QY 597 AGGAATGCGGAGGAAAAGACACATATACATACGCTGCTGCGCCGAGCCCTACGTGGA 656
DB 1835 GGGTGTGCGCGGCAACGTAACGAGATCTATTACAACTGCTGCTCCGCGGAACCTATAGA 1894
QY 657 CGTCACCTTCACCATCATGATGAAGAAGACGAACCTTGTACTTCTTCAACCTGATCGT 716

Db 1895 CATCACCTTCGCCATCATCATCCGCCGACGAACACTGTACTATTCTTCAACCTGATCAT 1954
QY 717 CCGGTGGTGTCTGATCTCATCTGATGATCGCTTCCTCGGCTTCACACTGCCACGACTCCGG 776
Db 1955 ACCTTGTGTAATGATTCCTCCATGCTTCTGCTGGATTCACCTGCGCGGAGATTCGG 2014
QY 777 AGAGAAACTCACACTTGGAGTCACTATTTCTATCTGCTGACGGTGTTCCTCAACCTGGT 836
Db 2015 TGAATAATTATCGCTGGTGTCTTACCATCTTGTCTGCTGACCGTGTCTTCTGAATATGGT 2074
QY 837 AGCGGAGACCTTCCACAGGCTCTCCGACGCTATATCCCTCTGT 877
Db 2075 TGCCGAGACATGCCGGCTACTTCCGATGCGGTGCCATTGT 2115

RESULT 6

AAC58395

ID AAC58395 standard; cDNA; 1509 BP.

XX

AC AAC58395;

XX

DT 29-JAN-2001 (first entry)

XX

DE Human PRO2145 nucleotide sequence SEQ ID NO:76.

XX

Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
proliferation; tumorigenesis; identification; cancer; cytostatic;
neotropic; neuroprotective; antiinflammatory; immunosuppressive;
immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
neural disorder; glial disorder; astrocytal disorder; angiogenic;
hypothalamic disorder; glandular disorder; macrophagal disorder;
epithelial disorder; stromal disorder; blastocoealic disorder;
inflammatory disorder; immunologic disorder; ss.

XX

OS Homo sapiens.

XX

PN WO200053755-A2.

XX

PD 14-SEP-2000.

XX

PF 06-JAN-2000; 2000WO-US00376.

XX

PR 08-MAR-1999; 99WO-US05028.

PR

02-JUN-1999; 99WO-US12252.

PR

23-JUN-1999; 99US-0141037.

PR

07-JUL-1999; 99US-0143048.

PR

26-JUL-1999; 99US-0145698.

PR

30-NOV-1999; 99WO-US28313.

PR

20-DEC-1999; 99WO-US30911.

PR

05-JAN-2000; 2000WO-US00219.

XX

(GETH) GENENTECH INC.

PA

Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;

PI

Watanabe CK, Wood WI;

XX

WPI; 2000-572270/53.

DR

P-PSDB; AAB24088.

XX

Thirty PRO polynucleotides encoding PRO polypeptides, useful in the

PT

treatment, diagnosis and prevention of cancer -

XX

Claim 50; Fig 57; 286pp; English.

PS

The present invention describes an isolated antibody that binds to

CC

one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,

CC

PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,

CC

PRO1025, PRO1030, PRO1097, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,

CC

PRO1281, PRO1283, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,

CC

PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell

CC

growth. The PRO polypeptides and nucleotides are useful in the

CC

treatment, diagnosis and prevention of cancer. The antibodies and other

anti-tumour compounds may be used to treat various conditions, including those characterised by overexpression and/or activation of the amplified PRO genes. Exemplary conditions or disorders to be treated with such antibodies and other compounds include benign or malignant tumours (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytic, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoeic disorders, and inflammatory, angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR sequences and hybridisation probes used in the isolation of the human PRO genes. AAC38367 to AAC58396 and AAB24057 to AAB24089 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

SQ Sequence 1509 BP; 297 A; 451°C; 429 G; 332 T; 0 other;

Query Match	25.1%;	Score 377.2;	DB 21;	Length 1509;
Best Local Similarity	55.2%;	Pred. No. 3.6e-95;		
Matches 811;	Conservative 0;	Mismatches 633;	Indels 24;	Gaps 3
Qy	33	GGCTTTTCGTGCCCCGCTATCGGAGCAAGGTCTCTCACGAGAGAGACTCCCTGAACGCCGTTGCT	92	
Db	42	GTCGCTCCTGCACGCTGCTCCCTGCAAGGCGAGTTCAGAGGAAGCTTTACAAGGAGCTGGT	101	
Qy	93	GGCGAACTACAACACCCCTGGAGCGACCGGTGCCCAACGAGAGCGAACCCTAGAGCTCAG	152	
Db	102	CAAGAACTACAATCCCTTGGAGAGCGCGTGCCCAATGACTCGCAACCACCTACCGCTCTA	161	
Qy	153	GTTCCGGCTTGACCTGGCAGCAAAATCATTTGAGCTGGACGAGAGAAATCAACTACTTTATAAC	212	
Db	162	CTTCTCCCTCGACCTCTCTGCAGATCATGAGCTGATGAGAGAACCAAGTTTTAAACAC	221	
Qy	213	CAATATATGGCTGCTGTGGAGTGGATGACTACAACCTGAGGTGGAACGACAGCGACTA	272	
Db	222	CAACATTTGGCTGCAATGTCTTGGACAGATCACTATTTACAGTGAATGTGTCAGAATA	281	
Qy	273	TGGCGGGTCAAGGACCTCAGGATFCACGCCCAACAAGTTGTGAAGCCGAGCGTCTTTAT	332	
Db	282	TCCAGGGGTGAAGACTGCTGTTTCCAGATGGCCAGATTTTGGAAACCAGACATTTCTTCT	341	
Qy	333	GTATAATAGTGCCTGACGAGGGTTTGGAGGGACCTACCAGACCACACTGGTGGTCAGAG	392	
Db	342	CTATAACAGTGTCTGATGAGCGCTTTTGACGCCACATTCACACTAACGTGTGGTGAATTC	401	
Qy	393	CGCGCGGAGTTGCCGTGTACGTGCCACCTGGCATATTCGAAGAGCACATCAAGATGGACAT	452	
Db	402	TTCTGGGCATTTGCCAGTACCTGCTCCAGGCGCATATTCGAAGTTCCTGCTACATCGATGT	461	
Qy	453	CGCGTGGTTTCCCTTTCGACAGCAACAACTGTGATATGAAGTTCCGTAGCTGGACATATGA	512	
Db	462	ACGCTGGTTTCCCTTTGATGTGCAGCACTGCAAACTGAAGTTTGGGTCTCTGGCTTACGG	521	
Qy	513	CGGCAATCAGTTGGATCTGTGTCTTAAAGATGAGGCGCGCGCATCTATCGGACTTCAT	572	
Db	522	AGGCTGGTCTTGGATCTGCAGATGCAGGA-----GCCAGATATCACTGGGTATAT	572	
Qy	573	AACAAATGGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAAGAACACAATAAACATACGC	632	
Db	573	CCGCAATGGAGAATGGGACCTAGTGGGAATCCCCCGGAAGAGGAGTGAAGGTTCTATGA	632	
Qy	633	GTGCTGCCCGAGCCCTACGTGGAGCTCACTTCCACCATCATGATAGAAGACGNAACCTT	692	
Db	633	GTGCTGMAAGAGCCCTACCCGATGTACCTTTCACAGTGACCATGGCCCGCAGGAGCGCT	692	
Qy	693	GTACTACTTCTCAACCTGTATCGTCCCGTGGCTGCTGCTCATCTCATGTGGCACTCCCTGG	752	
Db	693	CTACTATGGCCCTCAACCTGTGATCCCTCTGTGTGCTCATCTCCGCCCTCGCCCTGCTGGT	752	
Qy	753	CTTCACTACGCCACGAGCTCCGGAGAGAACTCACACTTGGAGTCACTATTCCTCTATC	812	
Db	753	GTTTCTGTCTCTTCAGATTTCCGGGAGAGAATTTCCCTGGGATAACAGTCTTACTCTC	812	

PA (PRAA) PHARMACIA & UPJOHN CO.
 XX Groppi VE, Wolfe ML, Berkenpas MB;
 XX WPI: 2001-061524/07.
 DR P-PSDB; AAB50012.
 XX Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT
 XX
 FS Example 5; Pages 60-61; 77pp; English.
 XX
 CC The present sequence is the coding sequence for wild-type human alpha7
 CC nicotinic acetylcholine gated ion channel. The human alpha7 ion channel
 CC was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)
 CC chimeric ligand gated ion channel (see AACS90382 and AAB50014). The
 CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
 CC in the present invention, resulting in preferential calcium ion
 CC conductance by the cells.
 XX
 SQ Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;

Query Match 24.9%; Score 374; DB 22; Length 1509;
 Best Local Similarity 55.1%; Pred. No. 2.9e-94;
 Matches 809; Conservative 0; Mismatches 635; Indels 24; Gaps 3;

Qy 33 GCGTTTCTGCTGCGGATCGGAGCAAGTCTCTCAGAGAGAGACTCTCTGAACGGTGGCT 92
 Db 33 GCGTTTCTGCTGCGGATCGGAGCAAGTCTCTCAGAGAGAGACTCTCTGAACGGTGGCT 92
 Qy 42 GTCCTCTGCTGCGGATCGGAGCAAGTCTCTCAGAGAGAGACTCTCTGAACGGTGGCT 101
 Db 42 GTCCTCTGCTGCGGATCGGAGCAAGTCTCTCAGAGAGAGACTCTCTGAACGGTGGCT 101
 Qy 93 GCGGAATACAAACACCTGAGGAGCGGTTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 152
 Db 93 GCGGAATACAAACACCTGAGGAGCGGTTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAG 152
 Qy 102 CAAGAAGTACAACTCCCTGGAGAGCGCGTGGCCAACTGCTCGCAACCACTCACCGTCTA 161
 Db 102 CAAGAAGTACAACTCCCTGGAGAGCGCGTGGCCAACTGCTCGCAACCACTCACCGTCTA 161
 Qy 153 GTTCGGCTTGACCTGAGCAAGTCAATGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 212
 Db 153 GTTCGGCTTGACCTGAGCAAGTCAATGAGTGGAGAGAGAGAGAGAGAGAGAGAGAGAG 212
 Qy 162 CTTCCTCCCTGAGCTGCTGAGATCATGGAGTGGATGAGAGAGAGAGAGAGAGAGAGAG 221
 Db 162 CTTCCTCCCTGAGCTGCTGAGATCATGGAGTGGATGAGAGAGAGAGAGAGAGAGAGAG 221
 Qy 213 CAATATATGCTGCTGCTGAGTGGATGAGTCAACCTGAGTGGAGAGAGAGAGAGAGAGAG 272
 Db 213 CAATATATGCTGCTGCTGAGTGGATGAGTCAACCTGAGTGGAGAGAGAGAGAGAGAGAG 272
 Qy 222 CAACATTTGCTGCAATGCTTGGACAGATCATTTTACAGTGGATGCTGAGATGCTGAGAT 281
 Db 222 CAACATTTGCTGCAATGCTTGGACAGATCATTTTACAGTGGATGCTGAGATGCTGAGAT 281
 Qy 273 TGGCGGGTCAAGGACCTCAGATCACGCCCAACAACTTGTGGAAGCGGAGAGAGAGAGAG 332
 Db 273 TGGCGGGTCAAGGACCTCAGATCACGCCCAACAACTTGTGGAAGCGGAGAGAGAGAGAG 332
 Qy 282 TCCAGGGTGAAGACTGCTGCTTCCAGAGATGGCCAGATTTGGAACCAACAGACATCTCT 341
 Db 282 TCCAGGGTGAAGACTGCTGCTTCCAGAGATGGCCAGATTTGGAACCAACAGACATCTCT 341
 Qy 333 GTATAATAGTCTGAGGAGGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 392
 Db 333 GTATAATAGTCTGAGGAGGTTTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 392
 Qy 342 CTATAACAGTCTGATGAGGCTTTGAGGCGACATTCACACTAACGTTGTTGTTGAATTC 401
 Db 342 CTATAACAGTCTGATGAGGCTTTGAGGCGACATTCACACTAACGTTGTTGTTGAATTC 401
 Qy 393 CGGCGGAGTTCCTGCTGAGTGGCCACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 452
 Db 393 CGGCGGAGTTCCTGCTGAGTGGCCACCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 452
 Qy 402 TTCTGGGCATTCGACGATACCTGCTCAGGATATTCAGAGTTCCTGCTACATCATGATG 461
 Db 402 TTCTGGGCATTCGACGATACCTGCTCAGGATATTCAGAGTTCCTGCTACATCATGATG 461
 Qy 453 CGCGTGTTCCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 512
 Db 453 CGCGTGTTCCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 512
 Qy 462 ACGCTGTTTCCCTTTGATGTCAGCACTGCAAACTGAAGTTTGGTCCCTGCTTACGG 521
 Db 462 ACGCTGTTTCCCTTTGATGTCAGCACTGCAAACTGAAGTTTGGTCCCTGCTTACGG 521
 Qy 513 CGGCAATCAGTTGATCTGTTGTTAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 572
 Db 513 CGGCAATCAGTTGATCTGTTGTTAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 572
 Qy 522 AGGCTGCTCTGATGTCAGATGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 572
 Db 522 AGGCTGCTCTGATGTCAGATGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 572
 Qy 573 AACAAATGGGAGTGGATCTAATGAAGATGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 632
 Db 573 AACAAATGGGAGTGGATCTAATGAAGATGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 632
 Qy 573 CCCCAGTGGAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 632
 Db 573 CCCCAGTGGAGATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 632
 Qy 633 GTGCTGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 692
 Db 633 GTGCTGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 692
 Qy 633 GTGCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 692
 Db 633 GTGCTGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 692
 Qy 693 GTACTACTTCTTCAACCTGATGCTGCCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 752
 Db 693 GTACTACTTCTTCAACCTGATGCTGCCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 752

Db 693 CTACTATGGCTCAACCTGCTGATCCCTCTGTGCTCATCTCCCTCCCTGCTGCTGGT 752
 Qy 753 CTTTACACACTGCGACCACTCCGAGAGAACTCACACTTGGAGTCACTATTTCTTCTATC 812
 Db 753 GTTCTCTCTCTGAGATTCGCGGAGAGATTTCCCTGGGAGATACAGTCTTACTCTC 812
 Qy 813 GCTGACGGTGTTCCTCAACCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 872
 Db 813 TCTTACCGTCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 872
 Qy 873 CTTGTTAGGAGCTACTTCAATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
 Db 873 ATTGATAGCCAGTACTTCCGACCACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
 Qy 933 TGTGTTGCTTCAATTTACCACTGATGATGATGATGATGATGATGATGATGATGATGAT 992
 Db 933 GGTGATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 992
 Qy 993 AAAATCAGTATTCCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
 Db 993 CAGAGTCTCTTCTGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1052
 Qy 1053 GATCACCAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1112
 Db 1053 CAAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1112
 Qy 1113 GTCGCTGAAGTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1172
 Db 1113 GAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1172
 Qy 1173 TCGGCTCTTAAACAGTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1232
 Db 1173 CTTGAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1230
 Qy 1233 CAGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1292
 Db 1231 GCCTGCTTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1288
 Qy 1293 GGTGAGCCATCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1352
 Db 1289 -----ACCGGACTTGGCCAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1337
 Qy 1353 GATGAGAGGCTGATGAGGAGCGGAGTGTGATGATGATGATGATGATGATGATGATGAT 1412
 Db 1338 CTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1397
 Qy 1413 TGTGATAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1472
 Db 1398 GGTGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1457
 Qy 1473 CTTGTTATCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1500
 Db 1458 CTTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1485

RESULT 8

AAT48239

ID AAT48239 standard; DNA; 1876 BP.

XX AAT48239;

XX 09-APR-1997 (first entry)

XX

XX

XX

XX Neuronal nicotinic acetylcholine receptor alpha-7 subunit DNA.

XX Neuronal nicotinic acetylcholine receptor; nAChR; neurotransmitter;

XX ligand-gated receptor; ds.

XX Homo sapiens.

XX

XX

XX Key Location/Qualifiers

XX CDS 73..1591

FT XX /*tag= a

PN WO9641876-A1.

XX 27-DEC-1996.

XX 07-JUN-1996; 96WO-US09775.

XX 07-JUN-1995; 95US-0484722.

XX (SIBI-) SIBIA NEUROSCIENCES INC.

XX Elliott KJ, Harpold MM;

PI WPI; 1997-065463/06.

DR P-PSDB; AAW09025.

XX Nucleic acids encoding nicotinic acetylcholine receptor sub-units -

PT used in screening to determine the effect of drugs on the receptor

XX Disclosure; Page 71-73; 108pp; English.

PS A DNA sequence (AA748239) codes for the alpha-7 subunit (AAW09025) of

CC the human neuronal nicotinic acetylcholine receptor (nAChR). Host

CC cells, esp. mammalian cells or amphibian oocytes, carrying alpha-7

CC nucleic acids, opt. in combination with other alpha and/or beta

CC subunit nucleic acids (see also AA748232-38, AA748240-41), express

CC recombinant nAChR subunits useful for identifying cpds. that

CC modulate the activity of human nAChRs.

XX Sequence 1876 BP; 369 A; 553 C; 531 G; 423 T; 0 other;

SQ

Query Match 24.9%; Score 374; DB 18; Length 1876;

Best Local Similarity 55.1%; Pred. No. 3.2e-94;

Matches 809; Conservative 0; Mismatches 635; Indels 24; Gaps 3;

QY 33 GGCTTTGCTGCGCGTATCGGAGCAAGTCTCTCAGAGAGAGACTCTCTGAACGCGTTGCT 92

DB 114 GTGCTCTCTGACGTCTGCTGCAAGGCGAGTTCCAGAGGAGCTTTTACAAGGAGCTGGT 173

QY 93 GGGCACTACACACCTCGAGGACCGGTGGCCACAGAGAGGAGGAGGAGTCTAGAGTCTAG 152

DB 174 CAGAACTACATCCCTTGGAGAGGCGCGTGGCCAAATGACTCGCAACCACTCACCCTCTA 233

QY 153 GTTGGCTGACCTTCAGCAAAATCATTTGACGTGGAGAGAGAAATCACTACTTATAAC 212

DB 234 CTCTCCCTGAGGCTCTCTGAGATCATGACGTGGATGAGAAACCAAGTTTAAACCAC 293

QY 213 CAATATATGGCTCTGCTGGAGTGGAAATGACTACACCTGAGGTGGAACAGCAGCAGTA 272

DB 294 CAACATTTGGCTGCAAAATGCTTGGACAGATCACTATTTACAGTGGAAATGTGTCAGAATA 353

QY 273 TGGCGGGTCAAGGACCTCAGGATACGCCCAAGTTGTGGAAGCGGAGCTCTCTAT 332

DB 354 TCAGGGGTGAAGACTGTCGTTCCAGATGGCCAGATTTGGAACCAACAGACTTCTCT 413

QY 333 GTATAATAGTGTGACGAGGTTTGGACGGGACCTACAGACCAAGCTGGTGGTTCAGAA 392

DB 414 CTATAACAGTGTGATGAGGCTTTGACGCCACATTTCCACACTTAAGCTGTGGTGAATTC 473

QY 393 CGCGGCGAGTGGCTGTAGTGGCCACCTGGCATATTTCAAGAGACATGCAAGATGACAT 452

DB 474 TTCTGGGCATTTGCCAGTACTGCTCCAGGCATATTTCAAGAGTTCTCTATCATGATGT 533

QY 453 CGCGTGTCTTCCCTTCGAGGACCAACACTGTGATATGAAGTTCTGGTGTGACATATGA 512

DB 534 ACGCTGGTTCCCTTTGATGTGACGACTGCAAACTGAAGTTTGGGTCTCTGCTTACGG 593

QY 513 CGCAATAGTGTGGTCTGCTAAAGATGAGGCGGCGGATCTATCGGACTTCAT 572

DB 594 AGGCTGGTCTTGGATCTCGATGCAGCA-----GGCAGATATCAGTGGCTATAT 644

QY 573 ACAAAATGGGAGTGTATCTTAATAGGAATGCCAGGCAAAAAGAACAAATAACATACGC 632

DB 645 CCCCAATGGAGATGGGACCTAGTGGGAATCCCGCAAGAGAGAGTGAAGGTTCCTATGA 704

QY 633 GTGCTGCCCGGAGCCCTACGTGACGTCACTTCAACCATCATGAAGAAGACGAACTT 692

DB 705 GTGCTGCAAGAGCCCTACCCGATGTCACTTCAAGTACAGTACCGCGGAGGAGCGT 764

QY 693 GTACTACTTCTTCAACCTGATGTCCTCCGTCGTCGTGATCTCATCATGATGGCACTCTCTCGG 752

DB 765 CTACTATGGCTCAACCTGCTGATCCCTGTGTGTCATCTCCGCTCTCGCTCTGCTGTGT 824

QY 753 CTTACACATGGCCACAGACTCCGGAGAGAAATCACTTGGAGTGCATTTCTTCTATTC 812

DB 825 GTTCTGCTTCTCTGAGATTCGGGGAGAGATTTCCCTTGGGATAAACAGTCTTACTCTC 884

QY 813 GCTGACGGTGTCTTCAACCTGATGTCGACAGACCTGCGCACAGGTCTCTCGAGCTATTC 872

DB 885 TCTTACCTGCTTCACTGCTGCTGCTGATCATGATCATGCCGCAACATCCGATTCGATACC 944

QY 873 CTTGTAGGAGCTACTTCAATTTGATCATGTTCAATGTTGAGTGTGCTGTGTGTTACTGAC 932

DB 945 ATTGATAGCCAGTACTTCCGACAGCACTATCATCTGTGGCTCTCTGCTGTGTGTTACTG 1004

QY 933 TGTGTTGTTACTCAATTTACCATTCGACAGCTGATATACATGAATGAATGCCACAGTGGAT 992

DB 1005 GGTGATGCTGCTGAGTACCAACACACACACCGGCGGAGAGTCCCAAGTGGAG 1064

QY 993 AAAATCAGTATTCCTTCAATGTTGTCATGATGTCGCAATGTCGAGGCGGAGGAGAA 1052

DB 1065 CAGAGTATCTTCTGAACTGTTGCGGTGTTCTTCCGCAATGAAGAGGCCCGGGAGGA 1124

QY 1053 GATCACCAAGAGACTTATAATGATGAACAGAGGATGAGGAGCTGGAATGAAGAGAG 1112

DB 1125 CAAGGTGCGCCGCTGTCAGACAGCAGCGGCTGTCAGCTTGGCCAGTGTGGAGAT 1184

QY 1113 GTCGTGAAAGTCTGCTGGGCAATTTCTAGATATGATGATGATCTTCAAGACAGGCGCC 1172

DB 1185 GAGCGCGTGGCGCGCGCCGCCAGCAACCGGAACTGCTGTATACATCGGTTCCGCGG 1244

QY 1173 TCCGCTCTTAACAGTACTGCTCGACCGGGAATTTGGGACCTGGGTGCTCAATATTCG 1232

DB 1245 CTTGACGCGGTGCACTGTGTCGACCCGCTCTGCGGTGATGTGTGGCGCAT--G 1302

QY 1233 CACGGAATTCGCTGGTGTGTCGTCGTCGTCAGATGGAAGAGCTGGGCGGCGGCT 1292

DB 1303 GCCTGCTCCCAACGACGATGAGCACTCTCTGACGCGGCGCAACCCCGGAGGGG-- 1360

QY 1293 GGGTAGCCACCATCGGAGCTGCACCTCATACTGAGAGAGCTGCACTTCAATCAGGCGCAG 1352

DB 1361 -----ACCGGACTTGGCAAGATCTTGGAGGAGTCCGCTACATTTGCCAATCG 1409

QY 1353 GATGAAGAGGCTGATGAGGAAGCGAGCTGATCAGCGACTTGAAGTTTGGTCCGATGT 1412

DB 1410 CTTCCGCTCCAGGAGCAAGAGCGGCTGTGACGAGAGTGAAGTTCGCGCTGTGT 1469

QY 1413 TCTTATAGTGTGCTGCTGTTTCACTATTTTCACTATTCATGAGAGTGTGAGTGT 1472

DB 1470 GGTGAGCCCTGTCCTCATGGCTTCTGCTCTTCCATCATCTGCAACATCATCTGCAACATCGGCAT 1529

QY 1473 CTTGTTATCGGACCGCATATCATCTGTG 1500

DB 1530 CTTGATGTGCGCTCCCACTTCGTGGAG 1557

RESULT 9
AAV44687

ID AAV44687 standard; cDNA; 1590 BP.

XX AAV44687;

XX 09-OCT-1998 (first entry)

DE V274T variant human alpha7 nAChR coding sequence.

XX Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer;
 KW neurodegeneration; enzyme dysfunction; affective disorder; therapy;
 KW immune dysfunction; diabetic neuropathy; Alzheimer's disease;
 KW schizophrenia; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 9..1517
 FT /*tag= a
 XX
 PN W09828331-A2.
 XX
 PD 02-JUL-1998.
 XX
 PF 22-DEC-1997; 97WO-US23405.
 XX
 PR 20-DEC-1996; 96US-0771737.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM;
 PI Roch J, Sullivan JP, Touma E;
 XX
 DR WPI; 1998-377593/32.
 DR P-PSDB; AAW69216.
 XX
 PT Nucleic acid encoding variant of human alpha7 nicotinic
 PT acetyl-choline receptor sub-unit - used to identify modulators of
 PT the receptor, potentially useful for treating neuro-degeneration,
 PT cancer, affective disorders etc.
 XX
 PS Claim 14; Fig 2; 44pp; English.
 XX
 CC This sequence encodes the V247T variant of human alpha7 nicotinic
 CC acetylcholine receptor (nAChR) subunit of the invention. Cells containing
 CC the DNA are used to express the protein and to identify modulators of
 CC alpha7 nAChR activity or cytoprotective agents, e.g. antisense
 CC compounds or antagonists that are potentially useful for treating
 CC neurodegeneration, enzyme dysfunction, affective disorders and immune
 CC dysfunction, such as cancer, post-herpetic neuralgia, diabetic
 CC neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
 CC psychosis and schizophrenia. Probes based on the DNA are used to detect
 CC the DNA in usual hybridisation or amplification tests, while monoclonal
 CC antibodies are used to detect the protein for diagnosis (in vitro or by
 CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR,
 CC the protein has about 100-fold greater sensitivity to cholinergic
 CC receptor agonists (nicotine or acetylcholine) and response to these
 CC agonists decays more slowly, but the wild-type inward rectification is
 CC retained.
 XX
 SQ Sequence 1590 BP; 322 A; 471 C; 449 G; 348 T; 0 other;
 Query Match 24.9%; Score 373.6; DB 19; Length 1590;
 Best Local Similarity 55.1%; Pred. No. 3.8e-94;
 Matches 808; Conservative 0; Mismatches 634; Indels 24; Gaps 3;
 35 CTTTCCTCCGCTATCGAGCAAGTCTCCAGGAAGAGACTCTGAAACGGTGTCTGG 94
 52 CTCCTCGACGTGTCCCTGCAAGCGGAGTTCAGAGGAAGCTTTACAAAGAGCTGTGCA 111
 95 CGAACTACAACACCTCGAGGACCGGTGGCCACGAGAGGAACCGCTAGAGGTCAAGT 154
 112 AGAATACAATCCCTTGAGAGGCCCGGTGGCCAAATGACTCGCAACCACTCAACGCTACT 171
 155 TCGGCTTGACCTTGACGAAATCATGTAGCTGGACGAGGAAGAACTACTATTATACCA 214
 172 TCTCCCTGAGCCTCTCGAGATCATGGACGTGGATGAGAAGAACCAAGTTTAAACCA 231
 215 ATATATGCTGCTGCTGGAGTGAATGACTACAACCTGAGTGGAAACGACGAGGATG 274
 232 ACATTGGCTGCAAAATGCTTGGACAGATCACTATTTACAGTGGAAATGTGTCAGAAAT 291

275 GCGGGGTCAAGGACCTCAGGATCACGCCCAACAAAGTTGTGGAAGCCGGACCTCTTATGT 334
 292 CAGGGGTGAAGACTGTTTCGTTTCCAGATGGCCAGATTGGAAACACAGACATTTCTCTCT 351
 335 ATAATAGTCTGACGAGGGTTTTCACGGGACCTACCAGACCAACGTTGTTGTCAGAGCG 394
 352 ATAACAGTGTGATGAGCGCTTTGACGCCACATTCACACATTAACGTTGTGTGAATCTT 411
 395 GCGCAGTTGCTGTACGTGCGACCTGGCATATTCAGAGACACATGCAAGATGACATCG 454
 412 CTGGCATTTGCCAGTACTGCTCCAGGCATATTCAGAGTTCTCTGCTACATCATGTAC 471
 455 CGTGGTTTCCCTTCGACGACCAACACTGTGTATATGAAGTTTCGGTAGCTGGACATATG 514
 472 GCTGGTTTCCCTTTGATGTGCAGCACTGCAAACTGAAAGTTTGGGTCTGCTTACGGAG 531
 515 GCAATCAGTTGGATCTGTTGCTAAAAGATGAGGAGCGGGCGGATCTATCGACACTTCAA 574
 532 GCTGCTCTTGGATCTGCAGATGCAGGA-----GGCAGATATCAGTGGCTATATCC 582
 575 CAAATGGGAGTGTATCTAATAGGAATGCCAGGCAAAAGAACACATAACATACACGGT 634
 583 CCAATGGAGATGGACCTAGTGGAAATCCCGCAAGAGAGTGAAGGTTCTATGAGT 642
 635 GCTCCCGGAGCCCTACGTGACGTACCTTTACCATCATGATGAAGAGACGAACCTTGT 694
 643 GCTGCAAGAGCCCTACCCGATGTACCTTTCACAGTGACCATGCGCGCAGGACACTCT 702
 695 ACTACTTCTCAACCTGATCGTCCGTCGCTGTGATCTCATGTCGACATCTCTCGCT 754
 703 ACTATGCGCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCGCTCGCCCTGCTGGGT 762
 755 TCACATGCCACACAGACTCCCGAGAGAAACACACTTGGAGTCACTATTCTTCTATCGC 814
 763 TCCTGCTCTCGAGATTCGGGGAGAGATTCCCTGGGGATACAGTCTTACTCTCTC 822
 815 TGACGGTGTTCCTCAACCTGTTAGCGAGACCTTGCCACAGGTTCTCGACGCTATFCCCC 874
 823 TTACACCTTCTCATGCTGCTGCTGAGATCATGCCCGCAACATCCGATTCGTTACCAT 882
 875 TGTAGGACGTACTTCAATTTGCATCATGTTTGGTAGCGTCTGCTGTGCTACTGACTG 934
 883 TGATAGCCCACTACTTTCGCCAGCACCATGATCATCGTGGGCTCTCGGTGGTGGAGCG 942
 935 TGTGGTACTCAATATACCACTCGACAGCTGATATACATGAATGCCACAGTGGATAA 994
 943 TGATCGTCTCAGTACCACCCACAGACCCCGCGGCGGCAAGATGCCAAGTGGACCA 1002
 995 AATCAGTATTCCTACAATGTTGCTGATGATGATGCGGAATGTCGAGGCCAGGGAAGA 1054
 1003 GAGTCATCTCTTGAACCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1062
 1055 TCACCGAAGACTATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1114
 1063 AGGTGCGCGCGCTGCGCAGCAAGCAGCGCGCTGCGCCTGCGCCTGCGCCTGCGCCTG 1122
 1115 CGTGAAGTCTGCTGCGGAATGTTCTAGATATTTGATGATGATGATGATGATGATGATG 1174
 1123 GCGCGTGGCG 1182
 1175 GCGCTCTTAACAGTACTGCTCGACCGGGAATTTGGGACCTTGGGTGCTCAATATATTC 1234
 1183 TGGACGGCGTCACTGTGCTCCGACCCCGACTGTTGGGTAGTGTGTGGCGCGCAT--GGC 1240
 1235 CGGATTTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1294
 1241 CTGCTCCCCCGACGACGATGAGCAGCTCTCTCGCGCGCGCGCGCGCGCGCGCGCGCG 1296
 1295 GTAGCCACCATCGCGAGCTGCACCTCTACTACTGAGAGAGCTGCACTTCAATCGCGCAG 1354
 1297 -----ACCGGACTTGGCAAGATCCTTGAGGAGGTCCGCTACATTTGCCAACCGCT 1347

QY 1355 TGAAGAAGGCTGATGAGGAAGCCGAGCTGATCAGCGACTGGAAGTTTGTGCGATGTTG 1414
 Db 1348 TCCGCTGCCAGGAGAAAGGAGCGGTCTGCGAGAGTGAAGTTTCCGCGCTGTGTGG 1407
 QY 1415 TTGATAGTTTTCCTGCTTCGTTACACACTTTTCAAAATCATCGGCAGACTGCTGCC 1474
 Db 1408 TGAACCGCTGTGCTCATGGCTTCTGCGTCTTCACCATCATCTGCACCATCGGCATCC 1467
 QY 1475 TGTATGCGCACCGCATATCATGTTG 1500
 Db 1468 TGATGTGCGCTCCCAACTTCGTGGAG 1493

RESULT 10

AAV12197
 ID AAV12197 standard; cDNA; 1876 BP.

XX AAV12197;
 AC
 XX
 DT 14-MAY-1998 (first entry)

Human neuronal nicotinic acetylcholine receptor alpha-7 subunit cDNA.

Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
 brain tissue; screening; NACHR; antibody; ds.

XX Homo sapiens.

PH Key Location/Qualifiers
 FT 73..1581
 CDS

FT /*tag= a
 FT /product= "neuronal nicotinic acetylcholine receptor
 alpha-7 subunit"

XX WO9420617-A2.

PN 15-SEP-1994.

XX 08-MAR-1994; 94WO-US02447.

XX 08-MAR-1993; 93US-0028031.

XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.
 PA (SIBI-) SIBIA NEUROSCIENCES INC.

PI Elliott KJ, Ellis SB, Harpold MM;

XX WPI; 1994-303024/37.

DR P-PSDB; AAW4153.

XX Human neuronal nicotinic acetylcholine receptor subunits and DNA -
 PT also transformed cells useful for screening cpds. which modulate
 PT activity of the receptor

XX Claim 8; Page 78-79; 99pp; English.

XX The present sequence encodes a human neuronal nicotinic acetylcholine
 CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta
 CC NACHR subunits may be used in a method of screening compounds to
 CC identify any which modulate the activity of human neuronal NACHR.
 CC Subunit specific antibodies may be used to monitor the distribution
 CC and expression density of various subunits in normal vs diseased brain
 CC tissues. Testing of single receptor subunits or specific receptor
 CC subunit combinations with a variety of potential agonists or antagonists
 CC provides information with respect to the function and activity of the
 CC individual subunits and should lead to the identification and design of
 CC compounds that are capable of very specific interaction with one or
 CC more receptor subtypes. The resulting drugs should exhibit fewer
 CC unwanted side effects than drugs identified e.g. screening with cells
 CC that express a variety of subtypes.

XX Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;

Query Match 24.9%; Score 373.6; DB 15; Length 1876;
 Best Local Similarity 55.0%; Pred. No. 4.1e-94;
 Matches 808; Conservative 1; Mismatches 635; Indels 24; Gaps 3;
 QY 33 GGCTTTGCTGCCGTATCGGAGCAAGTCTCTCAGGAGAAGAGACTCTCTGAACGGTGGCT 92
 Db 114 GTGCTCTCTGACGTGCTCCCTGCAAGCGAGTTCAGAGGAAGCTTTTACAAAGAGCTGGT 173
 QY 93 GCGAAATACACACACCTTGAGCGCGGTGGCGCAACGAGAGCGAAGCTAGAGGTGAG 152
 Db 174 CAAGAATCAATCCCTTGAGAGGCGCGTGGCCATGACTCGCAACCACTCACCGTCTA 233
 QY 153 GTTCGGCTTGACCTTGAGCAAAATCATGTGACGTGGAGAGAAATCAACTACTTATAAC 212
 Db 234 CTTCTCCCTGAGCTCTGAGATCATGGACGTGGATGAGAAGAACCAAGTTTAAACAC 293
 QY 213 CAATATATGGCTGCTGTTGGAGTGAATGACTACAACCTGAGTGGAAACACACAGGATA 272
 Db 294 CAACATTTGGCTGCAAAATGCTTTGGACAGATCACTATTTACAGTGAATGTGCAGATA 353
 QY 273 TGGCGGGGTCAAGGACTCAGGATCACGCCCAACAAGTTGTGGAAGCGGACGTCTCTAT 332
 Db 354 TCCAGGGGTGAAGACTGTTCTGTTCCAGATGGCCAGATTTGGAACACACACATCTTCT 413
 QY 333 GTATAATAGTGTGACGAGGGTTTTCACGGGACCTACACAGCAACAGTGGTGTGAGAAG 392
 Db 414 CTATAACAGTGTGATGAGCGCTTTGACGCCACATTTCCACACTAACTGTTGTGAATTC 473
 QY 393 CGCGGGAGTGGCTGTACGTGCCACTTGGCATATTTCAAGAGCACATGCAAGATGGACAT 452
 Db 474 TTTGGGCAATGGCAGTACGTGCTCCAGGCATATTTCAAGAGTTCCTGTGTACATCGATGT 533
 QY 453 CGCGTGGTTTCCCTTCGACGACCAACACTGTGTATATGAAGTTCGGTAGCTGGACATATGA 512
 Db 534 ACCTGGTTTCCCTTTGATGTGAGCACTGCAACTGAAAGTTTGGGTCTGGTCTTACGG 593
 QY 513 CGGCAATCAGTTGGATCTGGTGTAAAAGATGAGCGAGCGCGGATCTATTCGAGCTTCAT 572
 Db 594 AGGCTGGTCTTGGATCTGAGATGCAGGA-----GGCAGATATCATAGTGGCTATAT 644
 QY 573 AACAAATGGGAGTGGTATCTAATAGGAATGCCAGGCAAAAGAACACATATACATACGC 632
 Db 645 CCCCAATGGAGAATGGGACCTAGTGGGAATCCCGGCAAGAGAGTGAAGGTTCTATGA 704
 QY 633 GTCTGCCCGGAGCCCTAGCTGGACGTCACTTTCACCATCATATGAAGAGAGCAACCTT 692
 Db 705 GTCTGCAAGAGCCCTACCCCGATGTCACTTCACAGTACCATGCGCGCAGGAGGCT 764
 QY 693 GTACTACTTCTCAACCTGATCGTCCGCTGCTGATGATCTATCATGATGGCACTCTCTGG 752
 Db 765 CTACTATGGCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCTCTGCGCTGTGTGT 824
 QY 753 CTTACACTGCCACAGACTCCGGAGAGAAACTCACACTTGGAGTCACTATTTCTTATC 812
 Db 825 GTTCTCTCTCTGAGATTCGGGAGAGATTTCCCTGGGATACAGTCTTACTCTC 884
 QY 813 GCTGACGGTGTCTCTCAACCTGCTAGCGAGACCTGCCACAGGTCTCCGACGCTATPCC 872
 Db 885 TCTTACCGCTTCTATGCTGCTGCTGATGATCATGCCCGCAACATCCGATTCGGTACC 944
 QY 873 CTTGTTAGGACGACTTCAATTTGATCATGTTTCATGGTAGCGTCTGTGTGTACTGAC 932
 Db 945 ATTGATAGCCCACTTCTGCCACCACTGATCATCTCGTGGGCTCTCGTGTGTGTGAC 1004
 QY 933 TGTGGTGGTACTCAATTACCACCATCGACAGCTGATATACATGAATGCCACAGTGGAT 992
 Db 1005 GGTGATGCTGCTGAGTACCACTACCCAGCCCGGAGGAGAGTGCCTAAGTGGAC 1064
 QY 993 AAAATCAGTATTCTTCAATGTTGCTGATGCTGCAATGTGCGAATGTGCGAGCGCAGGAGAA 1052
 Db 1065 CAGAGTCATCTTCTGAACGTGGTGGTGTCTTCCGTAATGAAGAGCGCCGGGAGGA 1124
 QY 1053 GATCACCGAGAGACTATAATGATGAACACAGGAGTGGAGCTGGAATGAAGAGAG 1112

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Db 1125 CAAGTGGCCCGCTCCAGCACAAGCAGCGCGCTGCAGCCTGGCCAGTGGAGAT 1184
Qy 1113 GTCGTGGAAGTCCCTTGTGGGGAATGTTCTAGATATTGATGACTTTCAGACACGGGCC 1172
Db 1185 GAGCGCGTGGCGCGCGCGCCAGCAGCAAGGGAACCTGCTGATCATCGCTTCCGGGG 1244
Qy 1173 TCGCGCTCTAACAGTACTGCTCGACCGGGAATTTGGACCTGGTGCTCAATATTCG 1232
Db 1245 CTGGACGGCTGACACTGTGTCCCGACCCCGGACTCTGGGTAGTGTGGCCGCAT--G 1302
Qy 1233 CACGATTTCCGTGGTGGTTCGTCCTCCGTCACGATGGAAGACGTGGCGGGGGCT 1292
Db 1303 GCCTGCTCCCGACGACGATGAGCACCTCTGACGGCGGCAACCCCGGAGGGG-- 1360
Qy 1293 GGTAGCCACCATCGCGAGCTGCACCTCATATCATGAGAGCTGCAGTTTCATCAGCGCAG 1352
Db 1361 -----ACCGGACTTGGCGAAGATCCTGGAGAGTCCGTACATGCGAATCG 1409
Qy 1353 GATGAAGAAGCTGATGAGGAAGCGGAGCTGATCAGCGACTGGAAGTTTGTGCGATGGT 1412
Db 1410 CTTCGGCTGCCAGGACGAAAGCGAGCGGTCTGCAGCGAGTGGAAAGTTGCGCGCTGTGT 1469
Qy 1413 TGTTCATAGGTTTCCCTGTTCTGTTTCACACTTTTCACATCATCGGACAGTAGTGT 1472
Db 1470 GGTGACCGCTGTGCCCTCATGGCTTCTCGGTCTTACCACATCATCTGCACCATCGGAT 1529
Qy 1473 CTTGTTATCGGCACCGCATATATCGTG 1500
Db 1530 CTGATGTCGGCTCCCACTTCGTGGAG 1557

RESULT 11
ABV73248
ID ABV73248 standard; cDNA; 1876 BP.
XX
AC ABV73248;
XX
DT 22-JAN-2003 (first entry)
XX
DE Human neuronal NACHR alpha7 subunit encoding cDNA.
KW Human; neuronal; nicotinic acetylcholine receptor; NACHR; drug screening;
KW Immunochimistry; NACHR alpha7 subunit; gene; ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT CDS 73..1581
FT /tag= a
FT /product= "NACHR alpha7 subunit"
FT /note= "neuronal nicotinic acetylcholine receptor"
XX
PN WO200259266-A2.
XX
PD 01-AUG-2002.
XX
PF 29-OCT-2001; 2001WO-US50985.
XX
PR 01-NOV-2000; 2000US-0703951.
XX
PA (MERI ) MERCK & CO INC.
XX
XX Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;
PI P-PSDB; ABB82435.
DR WPI; 2002-698532/75.
XX
PT Cell comprising nucleic acids encoding human alpha and beta subunits of
PT neuronal nicotinic acetylcholine receptors, useful for in vitro
PT screening of a drug substance in a test system specific for humans
XX
PS Examples; Page 129-130; 143pp; English.

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XX The invention relates to a suitable host cell transfectd with an
CC isolated nucleic acid molecule comprising a sequence of nucleotides or
CC ribonucleotides that encodes at least one alpha or beta subunit of a
CC human neuronal nicotinic acetylcholine receptor (NACHR). The compositions
CC and methods of the present invention, which provide a means to prepare
CC synthetic or recombinant receptors and receptor subunits that are
CC substantially free of contamination from many other receptor proteins,
CC are useful for observing the effect of a drug substance on a particular
CC subtype to perform in vitro screening of the drug substance in a test
CC system that is specific for humans. The antibodies can be used in
CC immunochemistry and for diagnostic and therapeutic applications. The
CC present sequence represents a human neuronal NACHR alpha7 subunit
CC encoding cDNA.
XX
SQ Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;

Query Match 24.9%; Score 373.6; DB:24; Length 1876;
Best Local Similarity 55.0%; Pred. No. 4.1e-94;
Matches 808; Conservative 1; Mismatches 635; Indels 24; Gaps 3;

Qy 33 GGCTTTGCTGCCGCTATCGGAGCAAGGTCCTCAGGAGAAGAGACTCCTGGAACGGTTCCT 92
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Db 174 CAAGAAGTACAAATCCCTGGAGAGCGCGGTGCCAATGACTCGCAACCACTCACGCTCA 233
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Qy 273 TGGCGGGTCAAGGACCTCAGGATCAGCCCAACAAAGTTGTGAAGCGGAGCTTCCTTAT 332
Db 354 TCCAGGGTGAAGACTGTGCTTTCCAGATGGCCAGATTGGAACACAGACATCTTCT 413
Qy 333 GTATATAGTCTCAGCAGGCTTTTGGAGGACCTACAGACCAACAGTGGTGGTCAGAG 392
Db 414 CTATAACAGTCTGATGAGCGCTTTGACGCGCACATTCACACTAACGTTGGTGAATC 473
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Qy 513 CGCAATCAGTTGATCTGTTGCTTAAAGATGAGCGCGGCGCATCTATCGGACTTCAT 572
Db 594 AGCTGTGCTTGGATCTGCAGATGCAGGA-----GCACATATCATGTGGCTATAT 644
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Qy 633 GTGCTGCCCGAGCCCTACGTGGAGCTACCTTCACCATCATGATATAGAGAACGAACCTT 692
Db 705 GTGCTGCAAGAGGCCCTACCCGATGTCACTTCCAGTGACCATGCGCCGCGCAGAGCCT 764
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Qy 753 CTTTCACTGTCACAGACTCCGAGAGAACTCACACTTTGGAGTCACTATTTCTTCTATC 812
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D 825 GTTCTGCTTCTGAGATTCGGGAGAGATTTCCCTGGGATACAGCTTACTCTC 884
QY 813 GCTGACGCTGTTCTCAACCTGATCGTCCCGTGGTGTGATCTCATCGATGGCACTCCCTCGG 872
D 885 TCTTACCGTCTTCACTGCTGCTGGTGGTGGATCATGCCGCAACATCCGATTCGGTACC 944
QY 873 CTTGTTAGGAGCTACTTCAATTTGATCATCTGATGATGATGATGATGATGATGATGATGAT 932
D 945 ATTGATAGCCAGTACTTCCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1004
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D 1005 GGTGATGCTGCTGAGTACACACCTGAGACAGCTGATATACATGAATGCCACAGTGGAT 1064
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D 1065 CAGAGTATCTTCTGAACTGGTGGGCTGCTTCTCGAATGAAGAGCCCGGAGGA 1124
QY 1053 GATCACCAGGAAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1112
D 1125 CAAGTGGCGCCGCTGCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1184
QY 1113 GTCGTGAAAGTCTTGTGCGGATGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1172
D 1185 GAGGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1244
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D 1303 GCCTGCTCCCGCCACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1360
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D 1361 -----ACCGGACTTGGCAAGATCCTGGAGAGGTGCGCTACATTTGCCAATCG 1409
QY 1353 GATGAAGAAGCTGATGAGGAAGCGGAGCTGATCAGGAGCTGGAAGTTTGTCTGGATGGT 1412
D 1410 CTTCCGCTGCCAGAGCAAGCGAGCGGTCTGCGAGTGGAGTTGCGCGCTGTGT 1469
QY 1413 TGTGATAGGTTTTCCTGTTGTTTTCACATTTTTCACATATCATCGCAGTGTAGTGT 1472
D 1470 GGTGAGCGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1529
QY 1473 CTTGTTATCGCAGGATATCATCGTG 1500
D 1530 CTTGATGTCGGCTCCCAACTTCGTGGAG 1557
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RESULT 13

AAC90385

ID AAC90385 standard; cDNA; 1509 BP.

XX

AC AAC90385;

XX

DT 14-MAR-2001 (first entry)

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XX Mutant human alpha7 ligand gated ion channel coding sequence #1.
XX Human: alpha7 nicotinic acetylcholine gated ion channel; mutant;
KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
XX Homo sapiens.
XX WO200073431-A2.
XX 07-DEC-2000.
XX 25-MAY-2000; 2000WO-US11862.
XX 27-MAY-1999; 99US-0136174.
XX (PHAA ) PHARMACIA & UPJOHN CO.
XX Groppi VE, Wolfe ML, Berkenpas MB;
PI P-PSDB; AAB50015.
DR WPI; 2001-061524/07.
XX Special cell culture medium for treating cells and for inducing
PT mammalian cell lines to conduct calcium ions, comprising specified
PT concentrations of ions of sodium, calcium and potassium at specified pH
XX
XX Claim 50; Page 69; 77pp; English.
XX The present sequence is the coding sequence for a mutant human alpha7
CC nicotinic acetylcholine gated ion channel. The human alpha7 ion channel
CC was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)
CC chimeric ligand gated ion channel (see AAC90382 and AAB50014). The
CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
CC in the present invention, resulting in preferential calcium ion
CC conductance by the cells. The protein encoded by this sequence has the
CC wild-type threonine residue at position 230 substituted by a proline
XX residue.
XX Sequence 1509 BP; 296 A; 452 C; 429 G; 332 T; 0 other;
SQ
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Query Match 24.88; Score 372.4; DB 22; Length 1509;
Best Local Similarity 55.08; Pred. No. 8e-94;
Matches 808; Conservative 0; Mismatches 636; Indels 24; Gaps 3;

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QY 33 GGCTTTCTGCTGCGGCTATCGGAGCAAGTCTCTCAGAGAAGAGACTCTGAACGCTTGTCT 92
D 42 GTCGCTCTGCGAGCTGTCCCTGCAAGCGGAGTTCACAGGAGCTTTACAGGAGCTTGT 101
QY 93 GCGCACTACAACACCTGGAGCGACCGGTGGCCAGCAGAGCGGAGCGGTAGAGGTCTAG 152
D 102 CAAGAAGTACAATCCCTTGGAGAGCGCGGTGGCCAAATGACTCGCAACCACTCACCGTCTA 161
QY 153 GTTCGGCTTACCTTGCAGCAATCATTTAGGTGGAGGAGAGAGATCAACTACTTATTAAC 212
D 162 CTTCTCCTCTGAGCTCTCTGAGATCATGAGCTGGATGAGAAGAACCAAGTTTAAACCA 221
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D 282 TCCAGGGGTGAAGACTGTTCGTTTCCAGATGGCAGATTTGGAACACAGACATCTTCT 341
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Db 162 CTTCTCCTGAGCCTCTGCAGATCATGGAGCTGGATGAGAGAACCAAGTTTTTAACCAC 221
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Qy 273 TGGCGGGGTCAAGACCTCAGGATCAGCCCAACAAGTTGTGGAAGCCGACGTCCTTAT 332
Db 282 TCCAGGGGTGAAGACTTTCCTGTTCCAGATGGCCAGATTGGAAACCAACATCTCTCT 341
Qy 333 GTATATAGTCTGACAGAGGTTTGGACGGGACCTACAGACCAACGTCGTGTCAGAAG 392
Db 342 CTATAACAGTGTGAGGCTTTTGACGCCACATCCACATCAACGTTGTGTGAATTC 401
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Db 402 TTTCTGGSCATTGGCAGTACCTCCAGGCATATTCAAGAGTTCCTGCTACATCATGT 461
Qy 453 CGGCTGTTTCCCTTTCAGCACCAACACTGTGTATGAAGTTTCGGTAGCTGGACATATGA 512
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Db 1458 CCTGATGCTGCTGCCCAACTTCGTGGAG 1485

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Job time : 409.032 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2003, 00:04:15 ; Search time 5602.3 Seconds
(without alignments)
10975.350 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2	1503	100.0	3109	6	AX009614 Sequence
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4	770.2	51.2	2023	3	AF321447 Drosophil
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9	654	43.5	2110	3	AF321449 Drosophil
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19	377.2	25.1	1509	9	HSNACHRA7 H.sapiens m
20	377.2	25.1	1916	9	AF385585 Homo sapi
21	377.2	25.1	1977	9	HSU40583 Human alpha
22	376.8	25.1	1551	4	BT47 B.taurus mr
23	376.4	25.0	2106	10	RATNARAD L31619 Rattus ratt
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29	374	24.9	1876	6	AX1719088 Sequence
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31	374	24.9	2088	10	AF225980 Mus muscu
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ALIGNMENTS

RESULT 1
AF143847

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AF143847 3029 bp mRNA linear INV 27-MAY-1999
Heliothis virescens putative nicotinic acetylcholine receptor alpha
7-2 subunit mRNA, complete cds.

AF143847
AF143847.1 GI:4895006

Heliothis virescens (tobacco budworm)

Heliothis virescens

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.

1 (bases 1 to 3029)
Schulte,T., Oellers,N. and Adamczewski,M.

Pred. No. is the number of results predicted by chance to have a

TITLE Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha subunits

JOURNAL

Unpublished

2 (bases 1 to 3029)

Schulte, T., Oellers, N. and Adamczewski, M.

Direct Submission

Submitted (19-APR-1999) 2F-BTB, Bayer AG, Bldg. Q 18., Leverkusen

51368, Germany

FEATURES

Location/Qualifiers

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7-2 subunit"

/protein_id="AAD32698.1"

/db_xref="GI:4895007"

/translation="MAPMLAALALLPVSEQGPHEKRLNALLANVTLERPVANE

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CDMKFGSWTDGNQDLVLKDEAGDLSDFITNGEWYLIIGMPKKNTITYACCEPYV

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NLVAETLPQVSDAIPLLCTYENIMFVASSVLTIVLVNHYHRTADTHEPMOWIKSV

FLWETLPLMSRQKKTTRKTIMNTRMRELEKERSKSLLANVLDIDDDFRGPP

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BASE COUNT 908 a 586 c 718 g 817 t

ORIGIN

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Best Local Similarity 100.08; Pred. No. 0;

Matches 1503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 95 ATGGCCCCATATGTTGGCGCCCTGGCGCTGCTGGCTTTCCTGCGCTATCGGAGCAAGT 154

QY 61 CCTCAGAGAGAGACTCCTGAACGGTTCCTGGGAACTACACACCCCTGGAGCGCG 120

DB 155 CCTCAGAGAGAGACTCCTGAACGGTTCCTGGGAACTACACACCCCTGGAGCGCG 214

QY 121 GTGGCCAAAGAGAGCAACCGCTAGAGTTCAGGTTTCGGCTTTCAGCTTCAGCAAAATCAT 180

DB 215 GTGGCCAAAGAGAGCAACCGCTAGAGTTCAGGTTTCGGCTTTCAGCTTCAGCAAAATCAT 274

QY 181 GACGTGGACGAGAGAAATCAACTACTTATAACCAATATATGCTGTGCTGGAGTGGAA 240

DB 275 GACGTGGACGAGAGAAATCAACTACTTATAACCAATATATGCTGTGCTGGAGTGGAA 334

QY 241 GACTACAACTTGGAGTGAACGACGAGTATGGCGGGTCAAGGACCTCAGATCAGC 300

DB 335 GACTACAACTTGGAGTGAACGACGAGTATGGCGGGTCAAGGACCTCAGATCAGC 394

QY 301 CCCAACAAAGTGTGGAACCGGACGCTCTTATATATATAGTGTGACGAGGGTTCAGC 360

DB 395 CCCAACAAAGTGTGGAACCGGACGCTCTTATATATATAGTGTGACGAGGGTTCAGC 454

QY 361 GGGACCTACGACGAAACGTTGGTGTGAGAGCGGCGGACGTTGCCGTGTAGTCCACCT 420

DB 455 GGGACCTACGACGAAACGTTGGTGTGAGAGCGGCGGACGTTGCCGTGTAGTCCACCT 514

QY 421 GGCATATTCAGAGCACATGCAAGATGGACATCGCGTGGTTCCCTTCGACGACCAAC 480

DB 515 GGCATATTCAGAGCACATGCAAGATGGACATCGCGTGGTTCCCTTCGACGACCAAC 574

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QY 541 GATGAGCAGCGCGCGATCTATCGGACTTCAATAAATGGGAGTGGTATCTAATAGGA 600

DB 635 GATGAGCAGCGCGCGATCTATCGGACTTCAATAAATGGGAGTGGTATCTAATAGGA 694

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DB 755 ACCTTCACCATCATGATAAGAGACGACCTTGTACTTCTTCAACCTGATCGTCCG 814

QY 721 TGCCTGTGATCTCATCGATGGCCTCTCTCGGCTTCACACTGCCACACAGATCCGGAG 780

DB 815 TGCCTGTGATCTCATCGATGGCCTCTCTCGGCTTCACACTGCCACACAGATCCGGAG 874

QY 781 AAACCTACACTTGGAGTCACTATTCTTCTATCGCTGACGGTGTCTCTCAACCTGGTAGCC 840

DB 875 AAACCTACACTTGGAGTCACTATTCTTCTATCGCTGACGGTGTCTCTCAACCTGGTAGCC 934

QY 841 GAGACCTGCCACAGGCTCCGACGCTATCCCTCTGTAGGAGCTACTTCAATTGCATC 900

DB 935 GAGACCTGCCACAGGCTCCGACGCTATCCCTCTGTAGGAGCTACTTCAATTGCATC 994

QY 901 ATGTTCACTGTPAGCGTCTCTGTGCTACTGACTGTGTGTGCTCAATTTACCAACATCGA 960

DB 995 ATGTTCACTGTPAGCGTCTCTGTGCTACTGACTGTGTGTGCTCAATTTACCAACATCGA 1054

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AX009614

LOCUS

AX009614

3109 bp

DNA

linear

PAT 06-SEP-2000

AF321447 2023 bp mRNA linear INV 29-APR-2002
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 DEFINITION subunit variant type III (nAcRalpha-30D) mRNA, complete cds,
 alternatively spliced.
 AF321447
 AF321447.1 GI:20152848
 Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
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 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 2023)
 GRAUO,M., REENAN,R.A., CULETTO,E. and SATTELLE,D.B.
 Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
 Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster. Identify a
 New and Highly Conserved Target of Adenosine Deaminase Acting on
 RNA-Mediated A-to-I Pre-mRNA Editing
 Genetics 160 (4), 1519-1533 (2002)
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 11973307
 2 (bases 1 to 2023)
 GRAUO,M. and SATTELLE,D.B.
 Direct Submission
 TITLE Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
 Genetics Unit, University of Oxford, South Park Road, Oxford OX1
 30X, UK
 JOURNAL Location/Qualifiers
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 Best Local Similarity 70.9%; Pred. No. 1.1e-193;

Matches 1058; Conservative 0; Mismatches 393; Indels 42; Gaps 1;
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LOCUS Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6
DEFINITION subunit variant type II (nAcRalpha-30D) mRNA, complete cds,
alternatively spliced.
ACCESSION AF321446
VERSION AF321446
KEYWORDS AF321446.1 GI:20152846.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 2023)
AUTHORS Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
TITLE Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
JOURNAL Genetics 160 (4), 1519-1533 (2002)
MEDLINE 21969411
PUBMED 11973307
REFERENCE 2 (bases 1 to 2023)
AUTHORS Grauso,M. and Sattelle,D.B.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
3QX, UK
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Number AE003626"
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AF321448
LOCUS
DEFINITION

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Qy 926 TACTGACTGTGTGTTACTCAATTACCACCATCGACAGCTGATATACATGAATGCCAC 985
Db 1370 TGTGACAGTAGTGGTGCTCAACTACCATCGACAGCGGACATTCACGAGATGCCAC 1429
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RESULT 9
AF321449
LOCUS
DEFINITION
Drosophila melanogaster 2110 bp mRNA linear INV 29-APR-2002
subunit variant type V (nAcRalpha-30D) mRNA, complete cds,
alternatively spliced.
ACCESSION
AF321449
VERSION
AF321449.1 GI:20152852
KEYWORDS
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 2110)
Grauso, M., Keenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalphea5, Dalphea6 and Dalphea7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)

MEDLINE 21969411
PUBMED 11973307
REFERENCE 2 (bases 1 to 2110)
AUTHORS Grauso, M. and Sattelle, D.B.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
3QX, UK

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Db 410 TGTGTGCTCTGTGATCTTCTGCGGATAATTAAGAAAGCTGTCAAGGACCTCATGAA 469
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Db 470 AGCGCTGCTGAACCATCTGCTGTCCACCTACAACTACGCTGGAGCGCCGCAATG 529

Best Local Similarity 64.68; Pred. No. 1.le-141; Matches 929; Conservative 0; Mismatches 460; Indels 48; Gaps 3;		
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Qy	304	AACAAGTTGTGGAACGCGAGTCTTATGTAATATAGTGTGACGAGGTTTTCGAGCGG 363
Db	671	CACAGACTATGGAACGAGCGTCTTATGTATACACAGCGGAGGTTTTCGAGCGG 730
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Qy	1324	CTGAGAGAGTGCAGTTTCATACGCGCAGGATGAAGAGGCTGATGAGGAGCGGAGCTG 1383
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LOCUS		3701 bp DNA linear PAT 18-JUN-2001
DEFINITION		Nucleic acid encoding insect actyl choline receptor subunit.
ACCESSION		E58347
VERSION		E58347.1 GI:13019346
KEYWORDS		JP 200023680-A/2.
SOURCE		Heliothis virescens (tobacco budworm)
ORGANISM		Heliothis virescens (tobacco budworm)
REFERENCE		1 (bases 1 to 3701)
AUTHORS		Martin, A., Nadjia, E. and Thomas, S.
TITLE		Nucleic acid encoding insect actyl choline receptor subunit
JOURNAL		Patent: JP 2000023680-A 2 25-JAN-2000;
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PR		04-MAY-1998 DE 19819829.9
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C12N15/09, A01K67/033, C07K14/705, C07K16/28, C12N1/21, C12N5/10, PC		C12Q1/68,
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ACCESSION
AJ554210
VERSION
AJ554210.1 GI:29466436
KEYWORDS
nAcRalpha-18C gene; nicotinic acetylcholine receptor subunit Dalpha7.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1. (bases 1 to 1683)
Mullar, N.S.
AUTHORS
Direct Submission
TITLE
Submitted (31-MAR-2003) Mullar N.S., Department of Pharmacology, University College London, Gower Street, London, WC1E 6BT, UNITED KINGDOM
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QY 117 ACCGGTGGCCAGCAGAGCGCTAGAGGTGAGGTTCGGCTTGCACCTTGCAGCAAT 176
DB 1272 TCCGCTTCATGAATCGACCGCTTACATTAAGCTTTGGTTTAACTTTAATGCAAT 1331

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 Qy 1275 AGACGTGGCGGGCGGGTGGGTAGCCA-----CCATCGCGAGCTGCACCTCATACT 1325
 Db 2472 TGGCGTCAACCATCATACGTGCATCAATCATCACTCAATGAATATAGTTTAACTCT 2531
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 RESULT 15
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 subunit (nAcRalpha34E) mRNA, nAcRalpha34E-B allele, complete cds,
 alternatively spliced.
 ACCESSION AY036613
 VERSION 1
 KEYWORDS AY036613.1 GI:20340268
 SOURCE Drosophila melanogaster (fruit fly)
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 2834)
 Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
 Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
 Dalp3a5, Dalp3a6 and Dalp3a7, in Drosophila melanogaster Identify a
 New and Highly Conserved Target of Adenosine Deaminase Acting on
 RNA-Mediated A-to-I Pre-mRNA Editing
 Genetics 160 (4), 1519-1533 (2002)
 JOURNAL 21969411
 MEDLINE 11973307
 PUBMED
 REFERENCE 2 (bases 1 to 2834)
 Grauso, M. and Sattelle, D.B.
 Direct Submission
 TITLE Submitted (26-MAY-2001) MRC-FGU Human Anatomy and Genetics,
 University of Oxford, South Parks Road, Oxford OX1 3QX, UK
 JOURNAL
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 generates a loss of reading frame and a truncated
 polypeptide; alternatively spliced"
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 Query Match 27.4%; Score 412.4; DB 3; Length 2834;
 Best Local Similarity 59.08; Pred. No. 2.1e-98;
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 Qy 57 AGTCTCTCAGAGAGAGACTCTCTGAACCGGTCTCTGCGAATCAACACCCCTGGAGCG 116
 Db 1215 AGGATATCATGAAAAAGAGACTGTTACACGATCTTTTGGATCCTTATAATACACTAGAACG 1274
 Qy 117 ACCGGTGGCAACGAGAGCGNACCGCTAGAGGTACAGTTCGGCTTGACCTTGACGACCAAT 176
 Db 1275 TCCGGTTCTCAATGAATCGGACCCGTACAAATTAAGCTTTGGTTTAACTTTAAATGCAAAAT 1334
 Qy 177 CATTGAGCTGGACGAGAAGAAATCAACTACTTATTAACCAATATATGGCTGCTGTTGGAGTG 236
 Db 1335 TATCGATGTGGACGAGAAAAATCAATTTGCTAGTCACTAATGTGTGTTAAACTGGAGTG 1394
 Qy 237 GAATGACTACAACTGAGGTGGAACGACAGCAGTATGGCGGGGTCAAGGACCTCAGAGT 296
 Db 1395 GAACGACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTCGCAAT 1454
 Qy 297 CAGCCCAACAAAGTTTGGAAAGCCGAGCTCTTATGTATTAATAGTCTGACGAGGGTTT 356
 Db 1455 ACCGCGCATCGCATCTTGAAGCCGGAGCTGTCTGTATCAACAGTCCGGATGAGGGATT 1514
 Qy 357 TGACGGGACCTACCAGACCAACAGTGGTGGTCAGAAAGCGGCGGAGTTGCCCTGTACGTGCC 416
 Db 1515 TGACGGGACCTACCAGACGACGTGGTGGTGGTCGGAACAACGGCTGCTCTATACGTTC 1574
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 Db 1575 GCGGGGATCTTCAAGTCGAGCTGCAAGATCGACATCACGTGGTTCCTCTCGATGACCA 1634
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 Db 1635 GCGGTGGAGATGAAGTTCCGCACTTGGACCTACGACGAGTTCACGGTG----- 1683
 Qy 537 AAAAGATGAGCGAGCGCGCATCTATCGACTTATCAACAAATGGGAGTGTATCTAAT 596
 Db 1684 ----- 1683
 Qy 597 AGGAATGCCAGGCAAAAAGAACACAATAACATAGCGCTGTGCCCCGAGCCCTACGTGGA 656
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 Db 1739 CAYCACCTTCGCCCATCATCATCCCGCCGACGAACACTGTACTATTCTTCAACCTGATCAT 1798
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 Db 1799 ACCTTGTGACTGATTGCTCCATGGCTTGCCTGGATTACCTCCGCGCAGATTCGGG 1858
 Qy 777 AGAGAAATCACACTTGGAGTCACTATTCTTCTATCGCTGACGGTGTTCCTCAACCTGGT 836
 Db 1859 TGAATAATATTCGTGGGTGTACCATCTTGTCTCGCTGACCTGCTTCTGAATATGGT 1918
 Qy 837 AGCGGAGACCTGCCACAGGTCTCCGAGCTATCCCCCTGTGAGGAGTACTTCAATTG 896
 Db 1919 TGCCGAGACAATCCCGCTACTTCCGATCGGTGCCATTCGTGGTACATATTTCAATG 1978
 Qy 897 CATCATGTTCTAGTGTGCTGTGTTGACTGACTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 956
 Db 1979 CATAAATGTTTGTGTAGCTTTCATCCGTTGTGTCAACGATTTTAATAATTAATTAATTAATCA 2038

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:20 ; Search time 47.4386 seconds
(without alignments)
2698.100 Million cell updates/sec

Title: US-09-303-232-4
Perfect score: 2665
Sequence: 1 MGRARRSHLAAPAGLLLLL.....LFTTIATLAVLLSAPHIMVS 496

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriopl:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2665	100.0	496	5 Q9XZ13	Q9XZ13 heliothis v
2	2064.5	77.5	807	5 Q8T7V5	Q8T7V5 drosophila
3	2046.5	76.8	545	5 Q9VW19	Q9VW19 drosophila
4	1803.5	67.7	501	5 Q9XZ14	Q9XZ14 heliothis v
5	1795.5	67.4	494	5 Q8T7S2	Q8T7S2 drosophila
6	1792.5	67.3	494	5 Q8T7S1	Q8T7S1 drosophila
7	1790.5	67.2	494	5 Q8T7S3	Q8T7S3 drosophila
8	1774	66.6	509	5 Q8T7S0	Q8T7S0 drosophila
9	1769	66.4	523	5 Q8T7R9	Q8T7R9 drosophila
10	1484.5	55.7	534	5 Q9VL79	Q9VL79 drosophila
11	1371	51.4	525	5 Q8TPE2	Q8TPE2 drosophila
12	1279	48.0	273	5 Q9VJT9	Q9VJT9 drosophila
13	1242	46.6	502	11 Q9JHD6	Q9JHD6 mus musculus
14	1219.5	45.8	513	13 O03481	O03481 gallus gall
15	1141	42.8	461	5 P91197	P91197 caenorhabdi
16	1113	41.8	480	5 Q81932	Q81932 caenorhabdi

17	1106.5	41.5	335	5 Q9NKD1	Q9NKD1 drosophila
18	1058.5	39.7	554	5 Q62083	Q62083 caenorhabdi
19	1055.5	39.6	542	5 Q18556	Q18556 caenorhabdi
20	994	37.3	523	5 Q46128	Q46128 heliothis v
21	975.5	36.6	537	5 Q9U941	Q9U941 myzus persi
22	972	36.5	515	5 Q46133	Q46133 locusta mig
23	962	36.1	537	5 Q8MUR0	Q8MUR0 apis mellif
24	960	36.0	536	5 Q8ROY9	Q8ROY9 aphysia cal
25	956.5	35.9	509	5 Q8MM21	Q8MM21 aphys gossy
26	956.5	35.9	567	5 Q9VC74	Q9VC74 drosophila
27	951	35.7	536	5 Q8T9S0	Q8T9S0 aphysia cal
28	949.5	35.6	509	5 Q9NFX8	Q9NFX8 myzus persi
29	947	35.5	568	5 Q9NFR5	Q9NFR5 drosophila
30	942.5	35.4	552	5 P91765	P91765 myzus persi
31	940.5	35.3	512	11 Q91X60	Q91X60 mus musculu
32	937.5	35.2	545	5 Q96631	Q96631 heliothis v
33	932	35.0	499	11 Q8VHH6	Q8VHH6 mus musculu
34	929	34.9	540	5 Q46134	Q46134 locusta mig
35	928	34.8	499	11 Q8R4G9	Q8R4G9 mus musculu
36	928	34.8	504	11 Q8BV44	Q8BV44 mus musculu
37	926	34.7	531	5 Q96632	Q96632 heliothis v
38	924	34.7	495	11 Q8R493	Q8R493 mus musculu
39	923	34.6	517	5 Q96633	Q96633 heliothis v
40	913	34.3	497	5 Q46135	Q46135 locusta mig
41	911.5	34.2	532	5 Q9U940	Q9U940 myzus persi
42	908	34.1	595	5 P91764	P91764 myzus persi
43	907	34.0	494	11 Q8K0A7	Q8K0A7 mus musculu
44	903.5	33.9	501	11 Q9R291	Q9R291 mus musculu
45	903.5	33.9	501	11 Q8BGP7	Q8BGP7 mus musculu

ALIGNMENTS

RESULT 1

Q9XZ13 ID Q9XZ13 PRELIMINARY; PRT; 496 AA.
AC Q9XZ13;
DT 01-NOV-1999 (TREMREL. 12, Created)
DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
DT 01-MAR-2003 (TREMREL. 23, Last annotation update)
DE Putative nicotinic acetylcholine receptor alpha 7-1 subunit.
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte T., Oellers N., Adamczewski M.;
RT "Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Ce21 chan
to other insect nicotinic acetylcholine receptor alpha subunits.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF143846; AAD32697.1;
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 496 AA; 56347 MW; 8032FED8515A6210 CRC64;

Query Match 100.0%; Score 2665; DB 5; Length 496;
Best Local Similarity 100.0%; Pred. No. 1.3e-244;
Matches 496; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RT	New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing. *;	
RT	Genetics 160:1519-1533(2002).	
RL	- - SUBCELLULAR LOCATION: INTEGRAL; MEMBRANE PROTEIN (BY SIMILARITY).	
CC	- - SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.	
CC	EWBL; AF321447; AAM1394.1; ..	
DR	FlyBase; FBgn0032151; nAcR-alpha-30D.	
DR	InterPro; IPR006201; Neur_chan.	
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DR	InterPro; IPR006029; Neur_chan_memb.	
DR	Pfam; PF02931; Neur_chan_LBD; 1	
DR	Pfam; PF02932; Neur_chan_memb; 1.	
DR	TIGRfams; TIGR00860; LIC; 1.	
DR	PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.	
KW	Glycoprotein; Tonic channel; Postsynaptic membrane; Receptor;	
KW	Transmembrane.	
SQ	SEQUENCE 494 AA; 56113 MW; 48327537229573FF CRC64;	

Query Match	67.3%; Score 1792.5; DB 5; Length 494;
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Matches 341; Conservative 55; Mismatches 81; Indels 25; Gaps 5;	

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DB	63	LQQIIDVDENKQLLITNWLISLEWMDYLRWNETEYGVKDLRITPNKLMKPDVLMYNSA	122
QY	127	DEGFSTYPTNVVVRNNGSLYVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGYQL	186
DB	123	DEGFDGTYHTNIVVVKHSGSLYVPPGIFKSTCKMDITWFPDDQRCMKFGSWTYDGNQL	182
QY	187	DLQLODGGGDLSISFTVNGEWELIGVPGKNEIYNYCCPEYIDITFAVVIKRTLYEYF	246
DB	183	DLVLNSEDGGDLSDFITNGEYWLAMPEKNTIYACCPEDYDITFTIQIRRLTYEYF	242
QY	247	NLIIVPCVLIIASMLLGLTLPDPSGEKLSLGVTTILLSLTVFLNMVAETMPATSDAVPLIGT	306
DB	243	NLIIVPCVLIISSMLLGLTLPDPSGEKLTGVTILLSLTVFLNLVAETLPQVSDAIPLLGT	302
QY	307	YFNCIMFWASSVSTLIILNYHRRHADTHIEMSDWIRCVFLYWLPWVLRMSRPGSATTPP	366
DB	303	YFNCIMFWASSVYLTVVVLYNHRTADIHEMPEWIKSVFLQWLPIWLRMRGPRGKTRK	362
QY	367	PARVP-PPDLELRSSKSLANVLDDIDDFRHPQAQQPCCCRYRGGEENGALAA--	423
DB	363	TILLSNRMKLELERSKSLANVLDDIDDFRHTIS-----GSGTAIGSSASF	411
QY	424	-----HSCFGVDY-ELSLILKEIRVITDQMRKDDDEDADISRDWKFKFAMVVDRLCLI	473
DB	412	GRPTVEEHTAIGCNKHDLHLILKELQFITARMKADDEAELIGDKFKFAMVVDRLCLI	471
QY	474	IFTLFTIATLAVLLSAPHIMV	495
DB	472	VFTLFTIATVTLSSAPHIIV	493

RESULT 7	
Q8T7S3	PRELIMINARY; PRT; 494 AA.
ID	Q8T7S3;
AC	Q8T7S3;
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 23, Last sequence update)
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE	Nicotinic acetylcholine receptor Dalp6a subunit variant type I.
GN	NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Ephydroidea; Drosophilidae; Drosophila.
OX	NCBI_TaxID=7227;

[illegible]

RESULT 8

RESULT
08T750

	ID	Q1	Q2	Q3	Q4
AC	1	1	1	1	1

$$\frac{DT}{DT}$$

DT	DE
0	N

GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalphas5, Dalphas6 and Dalphas7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF321448; AAM13395.1; -;
DR FlyBase; FBgn0032151; nacr-alpha-30D.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
KW SEQUENCE 509 AA; 57887 MW; B8D8E0198E0C2BD CRC64;

Query Match 66.6%; Score 1774; DB 5; Length 509;
Best Local Similarity 66.0%; Pred. No. 7.1e-160;
Matches 341; Conservative 54; Mismatches 82; Indels 40; Gaps 6;

QY 8 SHLAAPAGLLLLCLLMPRGARC-GYHEKRLHLLHLLDHYNVLPRPVNVEDPLQSLGTL 66
DB 3 SPLPASLSLVLLIFLAIIKESCGPHEKRLNLLSTYNTLERPVANESPELVKFGTL 62
QY 67 LMQIIDVDEKNOILLITNWLKLEWDMNLRNWTSDFGVGDRLRVP 111
DB 63 LQIIDVDEKNOILLITNWLKLEWDMNLRNWTSDFGVGDRLRIT 122
QY 112 PHLWKPDVLMYNSADGFDSTYTNVVRNNGSLYVPPGIFKSTCKIDITWFPDQD 171
DB 123 PNKLWKPDVLMYNSADGFDSTYTNVVRNNGSLYVPPGIFKSTCKMDITWFPDQD 182
QY 172 CEMFGSWTYDGYQLDQLQDEGGDISFFVTNGEWELIGVPGKRNEIYNCCPEYIDI 231
DB 183 CEMFGSWTYDGNQLDLVNSEDDGDLSDFTITNGEWILLAMPKKNITVYACCEPIYDI 242
QY 232 TFVAVIRKTYLFFNLIVPCVLIIASMAILGFTLPDPSGKSLGVTILSLTVFLNWA 291
DB 243 TFTIQRRTLYLFFNLIVPCVLIISSMAILGFTLPDPSGKSLGVTILSLTVFLNVA 302
QY 292 ETMPATSDAVPLLTGYNCIMFVASSVSVTILNLYHRRHADTHMSDMTRCVFLYWL 351
DB 303 ETLFQVSDAIPLLGTGYNCIMFVASSVSVTILNLYHRRHADTHMSDMTRCVFLYWL 362
QY 352 WILRMSRPGSATPPPARVP-PPDLELRSSKSLANVLIDDDDFRHPQAOQPCCR 410
DB 363 WILRMRGRKTRTKTILNRMKLELKERSSKSLANVLIDDDDFRHTIS----- 414
QY 411 YRGEENGAGLAA-----HSCGVYD-ELSLILKEIRVITQMRKDEADISR 458
DB 415 ---GSQTAIGSSASFGRTTVEEHHTAIGCNHKLHLKELQITAMRMKRADEAELIG 471
QY 459 DWKFAAMVVDRLCLIFTLTIATLAVLLSAPHIMV 495
DB 472 DWKFAAMVVDRLCLIFTLTIATLAVLLSAPHIMV 508

RESULT 9
Q8T7R9

ID Q8T7R9 PRELIMINARY; PRT; 523 AA.
AC Q8T7R9;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor Dalphas6 subunit variant type V.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalphas5, Dalphas6 and Dalphas7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -I- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF321449; AAM13396.1; -;
DR FlyBase; FBgn0032151; nacr-alpha-30D.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
DR Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
KW SEQUENCE 523 AA; 59110 MW; 1C200AF74F87F841 CRC64;

Query Match 66.4%; Score 1769; DB 5; Length 523;
Best Local Similarity 64.4%; Pred. No. 2.2e-159;
Matches 342; Conservative 53; Mismatches 82; Indels 54; Gaps 6;

QY 8 SHLAAPAGLLLLCLLMPRGARC-GYHEKRLHLLHLLDHYNVLPRPVNVEDPLQSLGTL 66
DB 3 SPLPASLSLVLLIFLAIIKESCGPHEKRLNLLSTYNTLERPVANESPELVKFGTL 62
QY 67 LMQIIDVDEKNOILLITNWLKLEWDMNLRNWTSDFGVGDRLRVP 126
DB 63 LQIIDVDEKNOILLITNWLKLEWDMNLRNWTSDFGVGDRLRIT 122
QY 127 DEGFDSYPTNVVVRNNGSLYVPPGIFKSTCKIDITWFPDQDCEMKFGSWTYDGYQL 186
DB 123 DEGFDSYPTNVVVRNNGSLYVPPGIFKSTCKMDITWFPDQDCEMKFGSWTYDGNQL 182
QY 187 DLQLODEGGDISFFVTNGEWELIGVPGKRNEIYNCCPEYIDITFVAVIRKTYLFF 246
DB 183 DLVNSEDDGDLSDFTITNGEWILLAMPKKNITVYACCEPIYDITFVAVIRKTYLFF 242
QY 247 NLIYPCVLIIASMAILGFTLPDPSGKSLGVTILSLTVFLNVAETMPATSDAV----- 301
DB 243 NLIYPCVLIISSMAILGFTLPDPSGKSLGVTILSLTVFLNVAESPTTSDAVPLIGV 302
QY 302 -----PLLTGYNCIMFVASSVSVTILNLYHRRHADTHPE 337
DB 303 TILSLTVFLNVAETLPDPSDAIPLLGTGYNCIMFVASSVSVTILNLYHRRHADTHPE 362
QY 338 MSDWIRCVFLYWLPMWLRMSRPGSATPPPARVP-PPDLELRSSKSLANVLIDDD 396
DB 363 MPPWIKSVFLQWLPMWLRMSRPGSATPPPARVP-PPDLELRSSKSLANVLIDDD 422
QY 397 FRHPQAOQPCCRYYRGEENGAGLAA-----HSCGVYD-ELSLILKEIRVIT 444
DB 423 FRHTIS-----GSQTAIGSSASFGRTTVEEHHTAIGCNHKLHLKELQIT 471
QY 445 DQMRKDEADISRDKFAAMVVDRLCLIFTLTIATLAVLLSAPHIMV 495

ID AC Q9VJT9 PRELIMINARY; PRT; 273 AA.
 DT 01-MAY-2000 (TREMELrel. 13, Created)
 DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMELrel. 23, Last annotation update)
 DE CG498 protein.
 GN NCACR-ALPHA-34E OR NCACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR
 GN CG4498 OR CG16878.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Deichler A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flossler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Lasko P.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lassek P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferrieria S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirkas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Klomp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of Drosophila melanogaster genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003642; AAF53374.2; -;
 DR HSP; P58154; 119B.
 DR FlyBase; FBgn0028875; nACR-alpha-34E.
 DR InterPro; IPR006201; Neur_channel.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006029; Neur_channel_memb.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 SQ SEQUENCE 273 AA; 31655 MW; CA95F19953E37248 CRC64;
 Query Match 48.0%; Score 1279; DB 5; Length 273;
 Best Local Similarity 57.6%; Pred. No. 3.7e-113;
 Matches 247; Conservative 19; Mismatches 7; Indels 156; Gaps 4;
 QY 68 MQIDVDEKNOLLITNINLKLWNNNDNLRWNTSDFGYKDLRPVPHRLWKPDLVLYNSAD 127
 DB 1 MQIDVDEKNOLLITNINLKLWNNNDNLRWNTSDYGGVKDLRIPPHRIWKPDLVLYNSAD 60
 QY 128 EGFDSYTYTNVVRNNGSLVYPGIFKSTCKIDITWFPDDQRCMEKFGSWTYDGYQLD 187
 DB 61 EGFDTYQTNVVRNNGSLVYPGIFKSTCKIDITWFPDDQRCMEKFGSWTYDGFQV- 119
 QY 188 LQLQDEGGDISFVTNGENELIGVPGKRNEIYNCCEPYIDITFAVIRKTKTYYPFN 247
 DB 120 -----W--FSVPGKRNEIYNCCEPYIDITFAIIRRTLYYPFN 158
 QY 248 LIVPCVLIASMALLGFTLPPDSGKLSGLVTLISLTVFLNVAETMPATSDAVPLIGTY 307
 DB 159 LIIPCVLIASMALLGFTLPPDSGKLS-----LGTY 189
 QY 308 FNCIMFVASSVSVSTILINLHHRHADTHEMSDWIRCVFLYWLPLWLRMSRPGSATTPPP 367
 DB 190 FNCIMFVASSVSVSTILINLHHRNADTHEMSEW----- 223
 QY 368 ARVPPPPDLERRSKSLANVLDDIDDFRHPQAOQPCRCYRGGENGAGLAHSCF 427
 DB 224 ----- 223
 QY 428 GVDYELSLILKEIRVITDQMRKDDADISRDWKFAAMVDRCLIIETLETIATLAVL 487
 DB 224 -----LRKDDCNDIANDWKFAAMVDRCLIIETLETIATLAVL 264
 QY 488 LSAPHIMVS 496
 DB 265 LSAPHIIVS 273
 RESULT 13
 Q9JHD6
 ID Q9JHD6 PRELIMINARY; PRT; 502 AA.
 AC Q9JHD6;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)

Db 370 PK-----HPSLKNTENVL-----PGHPSNGNMNMYXHTMENPCPCQ-----NNDLG 413
Qy 419 AGLAAHSC-FCVDYE-----LSLKEIRVITDOMKDDDEDADISRDWFAA 464
Db 414 SKSKICVPLSENEHVOKKALMDTIPVIVKILIEVOFIAMFRKQDEGEICSEWFAA 473
Qy 465 MVVDRLCLIIITFTIATLAVLSAPHIM 494
Db 474 AVIDRLCLVAFTLFAICTTILMSADNFI 503

RESULT 15

P91197 ID P91197 PRELIMINARY; PRT; 461 AA.
AC P91197;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 52.7 kDa protein.
GN D2092.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Gattung S., Maggi L.;
RT "The sequence of C. elegans cosmid D2092.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL: U88167; AAB42223.1; -
DR WormPep; D2092.3; CE03102.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neu_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Hypothetical protein; Glycoprotein; Ionic channel;
KW Postsynaptic membrane; Transmembrane.
SQ SEQUENCE 461 AA; 52718 MW; 6182A7F827357B92 CRC64;

Query Match 42.8%; Score 1141; DB 5; Length 461;
Best Local Similarity 46.2%; Pred. No. 9.8e-100;
Matches 218; Conservative 85; Mismatches 121; Indels 48; Gaps 7;
Qy 34 EKRLHLLDHYVLEPVVNESDPLQLSEGLTLMQIIDVDYDEKNOLLITNIWKLWNDM 93
Db 26 ETKLFTDLKGYPLERPVONSQPLEVTKLFQQLLDYDEKNQIVSNAWLSYTFDH 85
Qy 94 NLRWNTSDFGKVDLRV--PHRLKPDVLMYNSADEGFDSTYPTNVVNRNNGSCLYVPP 151
Db 86 KLOWEPKYGIGIQRFPGSDHIWKPDVLLYNSAAEDFDSTFKSNLLIYHTCTVWIPP 145

Qy 152 GIFKSTCKIDITWFPFDDQRCMKFGSWTYDGYQLDLQDEGG-----DISSFTVNGEW 207
Db 146 GVLKFCQLDVTWFPFDDQRCMKFGSWTFHGVAIDLQIDDDTNGTQSMDLSTVYVNGEW 205
Qy 208 ELICVPCKRNEIYYNCCPEYIDITFAVVRRTKLYFFNLIVPCVLIASMALLGFTLPP 267
Db 206 QVISTNAKRVVSYKKCCPEYPTVNYLYLHRRRTLYYGFNLIIPSLDISMAILGFMFP 265
Qy 268 DSGEKLSGLVTILLSLTFLNVAETMPATSDAVPLIGTYFNCFIMFVASSVSTILN 327
Db 266 DAGEKITLEVITLLAIVFLLSMVSEPTTSEAVPLIGVFESCCMLVSVASVFTIVLN 325
Qy 328 YHHRHADTHEMSDWIRCVFLYWLPMVLRMSRPGSATPPPARVPPPPDLELRERSSKLL 387
Db 326 LHFRSADSHENMPLVRRVLEFLPWLFLMSRPG-----YKFKV 363
Qy 388 ANVLIDIDDDFRHPQAQOQPCCRYRGGEENGAGLAHSCFGVDYELSLIL-----KEIRV 442
Db 364 ANVIDSTDKM-PKKPKNPLDCNL-----PSNHAG-----YEAQILLHSHVHTELRR 408
Qy 443 ITDQMRKDDDEDADISRDWFAAMVVDRLCLIIITFTIATLAVLSAPHIM 494
Db 409 VVAFYKNEEHDRIQTDWRFAAMVVDRLCLIIITFTIATLAVLSAPHIM 460

Search completed: August 13, 2003, 15:29:09
Job time : 49.4386 secs

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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:55 ; Search time 10.386 Seconds
(without alignments)
2245.843 Million cell updates/sec

Title: US-09-303-232-4

Perfect score: 2665

Sequence: 1 MGRARRSHLAAPAGLLLLL.....LFTTIATLAVLLSAPHIMVS 496

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	1267	47.5	502	1	ACH7_CHICK
2	1246	46.8	502	1	ACH7_HUMAN
3	1241	46.6	502	1	ACH7_MOUSE
4	1232.5	46.2	502	1	ACH7_RAT
5	1218.5	45.7	498	1	ACH7_BOVIN
6	1201	45.1	498	1	ACH1_CAEEL
7	980.5	36.8	516	1	ACH1_MANSE
8	979	36.7	557	1	ACH1_SCHGR
9	960	36.0	503	1	ACH3_HUMAN
10	960	36.0	529	1	ACH2_HUMAN
11	959	36.0	528	1	ACH2_CHICK
12	956.5	35.9	567	1	ACH1_DROME
13	951	35.7	511	1	ACH2_RAT
14	936.5	35.1	495	1	ACH3_BOVIN
15	930	34.9	499	1	ACH3_RAT
16	926	34.7	576	1	ACH2_DROME
17	918.5	34.5	456	1	ACHA_CHICK
18	918	34.4	494	1	ACH6_HUMAN
19	917	34.4	496	1	ACH3_CHICK
20	908.5	34.1	491	1	ACHN_CHICK
21	906	34.0	461	1	ACHA_TORCA
22	904	33.9	622	1	ACHA_CHICK
23	903.5	33.9	498	1	ACHP_HUMAN
24	902.5	33.9	502	1	ACHN_HUMAN
25	902	33.8	495	1	ACHP_RAT
26	899	33.7	461	1	ACHA_TORCA
27	898.5	33.7	512	1	ACH3_CARAU
28	898	33.7	500	1	ACHN_RAT
29	896.5	33.6	457	1	ACHA_BOVIN
30	896.5	33.6	493	1	ACH6_RAT
31	893.5	33.5	519	1	ACH4_DROME
32	890	33.4	457	1	ACHA_RAT
33	889	33.4	457	1	ACHA_MOUSE

34	888	33.3	470	1	ACHP_CHICK
35	886.5	33.3	494	1	ACHN_CHICK
36	885.5	33.2	459	1	ACHN_CARAU
37	880	33.0	456	1	ACHA_BRARE
38	879.5	33.0	627	1	ACH4_HUMAN
39	876.5	32.9	457	1	ACH2_XENLA
40	874	32.8	521	1	ACH3_DROME
41	872	32.7	538	1	ACH8_CAEEL
42	867.5	32.6	630	1	ACH4_RAT
43	866.5	32.5	482	1	ACHA_HUMAN
44	858.5	32.2	452	1	ACH5_RAT
45	855.5	32.1	458	1	ACHO_HUMAN

ALIGNMENTS

RESULT 1
 ACH7_CHICK
 ID ACH7_CHICK STANDARD; PRT; 502 AA.
 AC P22770;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=91097796; PubMed=1702646;
 RA Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S.,
 Millar N., Valera S., Barkas F., Ballivet M.;
 RT "A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is
 RT developmentally regulated and forms a homo-oligomeric channel blocked
 RT by alpha-BTX.";
 RL Neuron 5:847-856(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=903115158; PubMed=2369519;
 RA Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;
 RT "Brain alpha-bungarotoxin binding protein cDNAs and MABs reveal
 RT subtypes of this branch of the ligand-gated ion channel gene
 RT superfamily.";
 RL Neuron 5:335-48(1990).
 RN [3]
 RP SEQUENCE OF 1-18 FROM N.A.
 RC STRAIN=White leghorn; TISSUE=Erythrocyte;
 RX MEDLINE=93049204; PubMed=1425587;
 RA Matter-Sadzinski L., Hernandez M.C., Roztocil T., Ballivet M.,
 Matter J.M.;
 RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor
 RT promoter develops during morphogenesis of the central nervous
 RT system.";
 RL EMBO J. 11:4529-4538(1992).
 RN [4]
 RP SEQUENCE OF 24-47.
 RC TISSUE=Brain;
 RX MEDLINE=85270494; PubMed=3860855;
 RA Conti-Tronconi B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
 Ray N., Raftery M.A.;
 RT "Brain and muscle nicotinic acetylcholine receptors are different but
 RT homologous proteins.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
 RN [5]
 RP MUTAGENESIS OF LEU-270.
 RX MEDLINE=92049732; PubMed=1719423;
 RA Recah F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
 Hussy N., Bertrand S., Ballivet M., Changeux J.-P.;

RT "Mutations in the channel domain alter desensitization of a neuronal
 RL nicotinic receptor.";
 RN Nature 353:846-849(1991).
 RP [6]
 RX MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
 RA MEDLINE=93024917; PubMed=1383829;
 RA Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
 RA Changeux J.-P., Bertrand D.;
 RT "Mutations in the channel domain of a neuronal nicotinic receptor
 RT convert ion selectivity from cationic to anionic.";
 RL Nature 359:500-505(1992).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
 CC IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC
 DR EMBL; X5295; CAA36543.1; .
 DR EMBL; X68246; CAA48317.1; .
 DR EMBL; X68586; CAA48576.1; .
 DR PIR; JN0113; JN0113.
 DR PDB; 1KC4; 17-APR-02.
 DR PDB; 1KL8; 17-APR-02.
 DR InterPro; IPR006029; Neu_channel_memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_Channel.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAWS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family; 3D-structure.
 FT SIGNAL 1 23
 FT CHAIN 24 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT DOMAIN 24 230
 FT TRANSMEM 231 255
 FT TRANSMEM 262 280
 FT TRANSMEM 296 317
 FT DOMAIN 318 469
 FT TRANSMEM 470 490
 FT DISULFID 150 164
 FT DISULFID 212 213
 FT CARBOHYD 46 46
 FT CARBOHYD 90 90
 FT CARBOHYD 133 133
 FT MUTAGEN 270 270
 FT CONFLICT 26 27
 FT SEQUENCE 502 AA; 56946 MW; 572325D4309AD2FD CRC64;
 Query Match 47.5%; Score 1267; DB 1; Length 502;
 Best Local Similarity 48.6%; Pred. No. 6.8e-100;
 Matches 249; Conservative 83; Mismatches 144; Indels 36; Gaps 6;
 QY 1 MGGARRSHLAAPAGLLLLCLLWPRGARGCVGHEKRLHLLHLLDHYNLERPVVNESDPLQ 60
 ||||| | ||||| | : | : ||| ||||| | : |||

Db 1 MGLRALMLWLLAAAGLV-----RESLQGEFORKLYKELLYKNYNPLRPVANDSQPLT 52
 QY 61 LSFGLTLMQIIDVDEKQNLITNIWKLKLEWMDMLRWNTSDFGYKDLRVPPHRLWKPDV 120
 Db 53 VYFTLSLQIMDVDEKQNLITNIWQLQWYTDHVLQWNVSEYPGVKVRFDPGLIWKPD 112
 QY 121 LMYSADGEGFSTPTNVVVRNNSCLYVPGIFKSTCKIDITWFPDDQCEMKFGSWT 180
 Db 113 LLNSADRRFDATFTNVLNVSNGHCQYLPPIKSSCYIDVRWFPDQVQCNLKFSGWT 172
 QY 181 YDGQDLQLODEGGDISSEFTVCEWELIGVPGKRNELIYVCCPEPIDITFAVVIK 240
 Db 173 YGWSLDLQMQE---ADISYISNGEWDVLGIPGRTESEFYECCKEPPDITFTVTMR 229
 QY 241 TLYYFNFLIVPCVLIASMALLFTLPDPSGKLSLGVITLLSLTVFLNVAETMPATSDA 300
 Db 230 TLYYGLNLLIPCVLISALLVFLPADSGEKISLGIITVLLSLTVFLNVAETMPATSD 289
 QY 301 VPLLGTYNCLMFVASSVSTLILNLYHHRHADTHEMSDWIRCVFLVLPVLRMSRPG 360
 Db 290 VPLIAQYFASPMIIVGLSVVTVIVLQVHHHPDGGKMPKTRVILLNWCAMFLRMKRP 349
 QY 361 SATPPPPARVPPDLELRSSKSLANVLD-----IDDDFRHPQAOQ 404
 Db 350 E-----DKVPACQHKORRCSLSMEMNTVSGQCSNGNMLYIGFRGLDGVHCTPTTDS 403
 QY 405 PQCCRYRGG--EENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDEADISRDWKF 462
 Db 404 GVICGRMTCSPTEENLHSGHPSEG-DPDLAKILEEVRYIANRFRDQDEBEAICNWK 462
 QY 463 AAMVVDRLCLIFLFTIATLAVLLSAPHIM 494
 Db 463 AASVVDRLCLMAFSVFTIICIGILMSAPNEV 494
 RESULT 2
 ACH7_HUMAN
 ID ACH7_HUMAN STANDARD; PRT; 502 AA.
 AC P36544; Q15826; Q96RH2; Q99555; Q9BXH0;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
 GN CHRNA7 OR NACHRA7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94195283; PubMed=8145738;
 RA Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
 RT "Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit
 RT from the SH-SY5Y cell line and determination of pharmacological
 RT properties of native receptors and functional alpha 7 homomers
 RT expressed in Xenopus oocytes.";
 RL Mol. Pharmacol. 45:546-554(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hippocampus;
 RA Logel J., Drebing C., Barnhart M., Antle C., Leonard S.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97062879; PubMed=8906617;
 RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
 RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
 RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
 RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
 RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
 RT beta 4 subunits";
 RL J. Mol. Neurosci. 7:217-228(1996).

[4] SEQUENCE FROM N.A.
 RX MEDLINE-97162233; PubMed-90092220;
 RA Groot Kormelink P.J., Luyten W.H.M.L.;
 RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
 RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
 RT line SH-SY5Y and/or IMR-32.";
 RL FEBS Lett. 400:309-314(1997).
 [5]
 RN REVISIONS.
 RA Groot Kormelink P.J., Luyten W.H.M.L.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 [6]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Epidermal Keratinocytes;
 RA Arredondo J., Grando S.A.;
 RT "Cloning cholinergic receptors in human keratinocytes.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 [7]
 RN SEQUENCE OF 17-502 FROM N.A.
 RC TISSUE=Brain;
 RA Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
 RA Lee J., Tian J., Giordano T.;
 RT "Cloning and sequence of the human $\alpha 7$ nicotinic acetylcholine
 RT receptor.";
 RL Drug Dev. Res. 30:252-256(1993).
 [8]
 RN SEQUENCE OF 24-502 FROM N.A.
 RC TISSUE=Retina;
 RX MEDLINE-94245214; PubMed-8188270;
 RA Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretto M.,
 RA Heinemann S.F.;
 RT "Molecular cloning and chromosomal localization of the human $\alpha 7$ -
 RT nicotinic receptor subunit gene (CHRNA7).";
 RL Genomics 19:379-381(1994).
 [9]
 RN SEQUENCE OF 118-129 FROM N.A.
 RX MEDLINE-21818878; PubMed-11829490;
 RA Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
 RT "A 3-Mb map of a large segmental duplication overlapping the $\alpha 7$ -
 RT nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
 RL Genomics 79:197-209(2002).
 [10]
 RN MASS SPECTROMETRY.
 RC TISSUE=Breast cancer;
 RX MEDLINE-21829512; PubMed-11840567;
 RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
 RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
 RA Zvelebil M.J.;
 RT "Cluster analysis of an extensive human breast cancer cell line
 RT protein expression map database.";
 RL Proteomics 2:212-223(2002).
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE AChR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
 CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- MASS SPECTROMETRY: MW=54157.68; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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 DR EMBL; X70297; CAA49778.1;

DR EMBL; U40583; AAB83561.1;
 DR EMBL; U62436; AAB40114.1;
 DR EMBL; Y08420; CAA69697.1;
 DR EMBL; AF385585; AAK68111.1;
 DR EMBL; L25827; NOT_ANNOTATED_CDS.
 DR EMBL; Z23141; CAA80672.1;
 DR EMBL; AF332758; AAK19515.1;
 DR PIR; G02259; G02259.
 DR PIR; I37185; ACHUA7.
 DR Genew; HGNC:1960; CHRNA7.
 DR MIM; 118511;
 DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan.; TAS.
 DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se.; TAS.
 DR GO; GO:000187; P:activation of MAPK; TAS.
 DR GO; GO:0006832; P:small molecule transport; TAS.
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neu_chan_LBD.
 DR InterPro; IPR006201; Neu_chan.
 DR Pfam; PF02931; Neu_chan_LBD; 1.
 DR Pfam; PF02932; Neu_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 22
 FT CHAIN 23 502
 FT BY SIMILARITY.
 FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-7 CHAIN.
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 231 230
 FT TRANSMEM 231 255
 FT TRANSMEM 262 280
 FT TRANSMEM 296 317
 FT DOMAIN 318 469
 FT TRANSMEM 470 490
 FT DISULFID 150 164
 FT DISULFID 212 213
 FT BY SIMILARITY.
 FT ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 46 46
 FT CARBOHYD 90 90
 FT CARBOHYD 133 133
 FT CONFLICT 11 11
 FT CONFLICT 58 58
 FT CONFLICT 134 134
 FT CONFLICT 364 364
 FT CONFLICT 375 375
 FT CONFLICT 409 413
 FT CONFLICT 502 502
 FT SEQUENCE 502 AA; 56449 MW; D94B3A482EAA0E42 CRC64;
 Query Match 46.8%; Score 1246; DB 1; Length 502;
 Best Local Similarity 46.0%; Pred. No. 4.1e-98;
 Matches 240; Conservative 86; Mismatches 126; Indels 70; Gaps 6;
 QY 12 APAGLLLLCLLPGRCAGCYHEKRLHLLHLLDHYNVLPRPVVNESDPLQSLGLTLMQII 71
 DB 4 SPGGVWLAAASLLHVSLOGEFQKLYKELVKNPLRPVANDSOPLTVFYLSLQIM 63
 QY 72 DYDEKNQVLTITNWLQMSWTDLQVNWSEYPCVKTVPFDPGQIKWPKDILLYNSADERED 131
 DB 64 DYDEKNQVLTITNWLQMSWTDLQVNWSEYPCVKTVPFDPGQIKWPKDILLYNSADERED 123
 QY 132 STYPTNVVNRNGSCLYVPPGIFKSTCKIDITWFPDDQCEMKFGSWYDGLDLQ 191
 DB 124 ATFTNVLVNSGHCQYLPFGIFKSSCYIDVRWFDPVQKCKLKFGSWYSGWSLQMQ 183
 QY 192 DEGGDGISSFTNGEWELGVGKNEIYVCCPEYIDITAVVRRRTLYFFNLVLP 251
 DB 184 E--ADISYIPNGEMDLVIGPKRSERYECKEYPDVFTVTRRTLYGLNLLP 240
 QY 252 CVLIASMLIGFTLPDSDGKISLGVITILLSLTVFLNVAETMPATSDAVPLIGTYFNCI 311
 DB 241 CVLISALALLVFLPADSGEKISLGVITILLSLTVFLNVAEIMPATSDVPLIAQYFAST 300
 QY 312 MFWASSVSTILILNHHRHADTHEMSDWIRCVFLYWLFWLWLRMSRPG----- 360

FT	TRANSEM	262	280	POTENTIAL.
FT	TRANSEM	296	317	POTENTIAL.
FT	DOMAIN	318	469	CYTOPLASMIC (POTENTIAL).
FT	TRANSEM	470	490	POTENTIAL.
FT	DISULFID	150	164	BY SIMILARITY.
FT	DISULFID	212	213	ASSOCIATED WITH RECEPTOR ACTIVATION
FT				(BY SIMILARITY).
FT	CARBOHYD	46	46	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	90	90	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	133	133	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	SEQUENCE	502 AA;	56631 NW;	C9312E5226D120E3 CRC64;
FSQ				
 Query Match 46.6%; Score 1241; DB 1; Length 502;				
Best Local Similarity 47.1%; Pred.No.1.le-97;				
Matches 243; Conservative 90; Mismatches 139; Indels 44; Gaps 6;				
Qy	1	MGRARRSHLAAPAGILLILLCLLWPRGARGCYHEKRLHLHLDHYNLVLRPPVYNESDP	LQ 60	
Ddb	1	MCGRRGGIWLALAAALLHV-----SLQGEFORRLKYELVKYNRPLERPVANDSQ	PLT 52	
Qy	61	LSFGTLTLMQIDVDENKNOLLITNIWIKLEWMDNMLRWNTSDGGVKDLRPPHRLWKPDV	120	
Ddb	53	VYFSLSLQIMDVDEKNQVLTTNIWLQSWTDHYLQWNMSEYPGVKNVRFPDGQIWKPDI	112	
Qy	121	LYMSADGEFDSTYPTNVVNRNGSCLVPGPCIFKSTCKIDITWPFFDDORCEMFSGWT	180	
Ddb	113	LYNSADERFDATFTHTVNLVNASGHCOYLPGCIFSSCIDYVRPFDFVOQCCLKFGWS	172	
Qy	181	YDGYQLDLQDEGGDISSFVTNGEWELIGVPGKRNEIYYNCCPEPIDITFAVVIRKK	240	
Ddb	173	YGGWSLDLQMQE---ADISSYTPNGEWDLMGIPGRNKEFYECCKEPYDVTYVTMMRR	229	
Qy	241	TLYEFNLIVPCVLIASWALLGFTLPDPSGKLSLGVTILLSLVFLNMVAETMATSDA	300	
Ddb	230	TLYYGNNLIIPCVLISALALLVFLPADSGEKISLTIGTVLLSLTFVMLLVAEIMATS	289	
Qy	301	VPLLGTGYINCFMWASSVYSTILINYHHRHADTHEMSDWTRCVFLXWLPWLVRMSRG	360	
Ddb	290	VELIAQYFASTMIIVGLSVVTVIVLYHHHPDGGKMPKWTRIILLNWCAMFLRMKRP	349	
Qy	361	SATTEPPARYPPPDLERBSKSLANVLIDDHFRHPQAQQOCCRYRGGE-----	415	
Ddb	350	EDKVAPCAQHCP-----RRCSLASV-BLSAGAPPTSNGNLLYIFRGLEGMHCA	398	
Qy	416	---ENGAGLIAAHSCFCV-----DYELSILIKELRVITDQMRKDDEDADISR	458	
Ddb	399	PTPDSVVCVGRILACSPTHDEHLMHGTHPSDGDPLAKILEEVRIANRFRCODESEVIC	458	
Qy	459	DKKFAMVDRCLLIIFLFTTIATLAVLLSAPHIM	494	
Ddb	459	EKKFAACVVDRLCLMAFSVFTICTIGILMSAPNFV	494	
 RESULT 4				
ACH7_RAT	ACH7_RAT	STANDARD:	PRT;	502 AA.
ID	ACH7_RAT			
AC	Q05941;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Neuronal acetylcholine receptor protein, alpha-7 chain precursor.			
GN	CHRNA7 OR ACRA7.			
RN	Rattus norvegicus (Rat).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=93147931; PubMed=7678857;			
RA	Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;			
RT	"Molecular cloning, functional properties, and distribution of rat			
RT	brain alpha 7: a nicotinic cation channel highly permeable to			

SQ SEQUENCE 498 AA; 57169 MW; E463ABB40AC9FA82 CRC64;

Query Match 45.1%; Score 1201; DB 1; Length 498;
Best Local Similarity 46.0%; Pred. No. 2.7e-94;
Matches 230; Conservative 89; Mismatches 151; Indels 30; Gaps 7;

QY 17 LLLLCULLPRGARGCGYHKKRLHLHLDHYNVLRPVVNESDPQLQSLFGLTLMQIIDVDEK 76
DB 6 LLTSCAILAAPTGLSGLQERLYEDLMRNYNLPRVANHSEPVTVHLKVALQOIIDVDEK 65

QY 77 NOLLITNWLKLEWMDNLRWNTSDFGKVKDLRVPVPHRLWKPDLVLMYNSADEGFSDFSTYPT 136
DB 66 NQVVYNWLDYTDNDYNLWDAEYGNITDVRFPAGKIWKDPVLLYNSVDTFNFDSTYQT 125

QY 137 NVVVRNNGSLYPPGIFKSTCKIDITWFPDQRCMEKFGSWTYDGYQLDQLQDEGG 196
DB 126 NMIVYSTGLVHWVPPGIFKISCKIDIQWFFDEQKCFKFGSWTYDGYKLDLQ-PATGGF 184

QY 197 DISSFTNGEWELIGVPGKREIYVNCPEPIYDITFAVIRKTLTYFFNLIVPCVLIA 256
DB 185 DISEYISNGEWALPLTVVERNEKFDCCPEYPDVHFYLMRRRTLYYGNLIMPCILTT 244

QY 257 SMALLGFTLPPDGSGLVGLTLLSLTVFLNVAETMPATSDAVPLLGTYFNCIMFVA 316
DB 245 LMTLLGFTLPPDAGEKITQITVLLSICFFLSIVSEMSPTSEAVPLLGITFCMIVVT 304

QY 317 SSVVSTILINLHRRHADTHEMSDWIRCVFLVPLWVLRMSRPGS----ATTTPPARVPP 372
DB 305 ASVFTVYVNLHRYTPETHDGCPTWRNLLLYWIPWILMKRGHNLTVASLPSLSTRP 364

QY 373 PDLERRSKSLANLVIDDDFRHQAQOPQC-CRYYRGEENGAGLAA-----423
DB 365 -----NRHSESLIRNIKDNEHLSRANSFADCRNLQYIMTQSVSNGLTSLGSPSTM 417

QY 424 HSCFGVDYELS-----LIL----KEIRVITDQMKDDEADISRDKFAAMVVDRLCLII 474
DB 418 ISSNGTTVDQSOATLHLRIYHELKIVTKRMIEGDKKEEQACNNWKFAMVVDRLCLYV 477

QY 475 FTLTITATLAVLLSAPHIM 494
DB 478 FTIFIVSTIGIFWSAPYL 497

RESULT 7

ACH1_MANSE STANDARD; PRT; 516 AA.

AC P51766;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholine receptor protein, alpha-like chain precursor (MARA1).
GN ARAL.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Sphingidae; Spinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98424077; PubMed=9753155;
RA Eastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Towner P.,
RA Reynolds S.E., Wolstenholme A.J., Wonnacott S.;
RT "Characterization of a nicotinic acetylcholine receptor from the
insect Manduca sexta";
RL Eur. J. Neurosci. 10:879-889(1998).
CC -I- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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CC -----

DR EMBL; Y0795; CAA70928.1; -
DR InterPro; IPR006029; Neu_channel_memb.
DR InterPro; IPR006202; Neu_chan_LBD.
DR InterPro; IPR006201; Neu_channel.
DR Pfam; PF02931; Neu_chan_LBD; 1.
DR Pfam; PF02932; Neu_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 516 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-
FT LIKE CHAIN.
FT DOMAIN 22 243 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 244 264 POTENTIAL.
FT TRANSMEM 274 294 POTENTIAL.
FT TRANSMEM 306 326 POTENTIAL.
FT DOMAIN 327 465 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 466 486 POTENTIAL.
FT DISULFID 149 163 BY SIMILARITY.
FT DISULFID 222 223 ASSOCIATED WITH RECEPTOR ACTIVATION
FT (BY SIMILARITY).
FT CARBOHYD 45 45 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 233 233 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 516 AA; 58720 MW; E7A71E8C45D13BD2 CRC64;

Query Match* 36.8%; Score 980.5; DB 1; Length 516;
Best Local Similarity 40.5%; Pred. No. 1.5e-75;
Matches 205; Conservative 75; Mismatches 159; Indels 67; Gaps 7;

QY 22 LLWPRGARGCYHEKRLHLLHLDHYNVLRPVVNESDPQLQSLFGLTLMQIIDVDEKNOLLI 81
DB 13 VLFATCGAGNPAKRLYDLDLLSNKLVLRPVVNSDALVRIKLSQLIDVNLKQIMT 72

QY 82 TNLWLEWMDNLRWNTSDFGKVKDLRVPVPHRLWKPDLVLMYNSADEGFSDFSTYPTVNVVR 141
DB 73 TNLWLEWMDNLRWNTSDFGKVKDLRVPVPHRLWKPDLVLMYNSADEGFSDFSTYPTVNVVR 132

QY 142 NNGSCLYVPPGIFKSTCKIDITWFPDQRCMEKFGSWTYDGYQLDQLQDEGG----- 196
DB 133 YTGVRVWRPPTAIYKSSCEIDVEYFPDQRCMEKFGSWTYDGYQLDQLQDEGG----- 192

QY 197 ---DISSFTNGEWELIGVPGKREIYVNCPEPIYDITFAVIRKTLTYFFNLIVPCV 253
DB 193 LGVDLSEFTSVSEWIDLEVPVNRNEFYCCDEPDITDITFNTRKRTLYFTVNLIPCM 252

QY 254 LIASMAALLGFTLPPDGSGLVGLTLLSLTVFLNVAETMPATSDAVPLLGTYFNCIMF 313
DB 253 GISFLTVLVFLPSDSGKSVLSISLLSLTVFLNVAETMPATSDAVPLLGTYFNCIMF 312

QY 314 MYASSVSTILINLHRRHADTHEMSDWIRCVFLVPLWVLRMSR-----359
DB 313 LDTFSCVTVVNLNVHFRSPQTHMTSPWRRVRIHVLPRLLVMRRPHYRLDPHRSFAGL 372

QY 360 -----GSATTPPPARVPP--PPDLERRSKSLANLVIDDDFRHQAQOP 405
DB 373 VTGAGETTLDWDESGVGPVAPRPPPCAPP-----LAPCAAC-----APAEAP 414

QY 406 QCCRYRGEENGAGLAAHSCFGVDELSLILKEIRVITDQMKDDEADISRDKFAAM 465
DB 415 ALCDALR-----RWHRC-----PELHKAIDGINVIADOTRKEESTRVKEDWYVAM 461

QY 466 VDRCLIIITFTIATLAVLLSAP 491
DB 466 VDRCLIIITFTIATLAVLLSAP 491

RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
 RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
 RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
 RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
 RT beta 4 subunits.";
 RL J. Mol. Neurosci. 7:217-228(1996).
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=97162233; PubMed=9009220;
 RA Groot Kormelink P.J., Luyten W.H.M.L.;
 RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
 RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
 RT expression of seven nAChR subunits in the human neuroblastoma cell
 RT line SH-SY5Y and/or IMR-32.";
 RL FEBS Lett. 400:309-314(1997).
 RN [5]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=99118870; PubMed=9921897;
 RA Rempel N., Heyers S., Engels H., Sleepers E., Steinlein O.K.;
 RT "The structures of the human neuronal nicotinic acetylcholine receptor
 RT beta2- and alpha3-subunit genes (CHRNA2 and CHRNA3).";
 RL Hum. Genet. 103:645-653(1998).
 RN [6]
 RN SEQUENCE FROM N.A. AND VARIANT LEU-21 INS.
 RX MEDLINE=21342809; PubMed=11450844;
 RA Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.;
 RT "Characterization of the human beta4 nAChR gene and polymorphisms in
 RT CHRNA3 and CHRNA4.";
 RL J. Hum. Genet. 46:362-366(2001).
 RN [7]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RX TISSUE=Lung;
 RC MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Stapleton L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Villalón D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Richardson S., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [8]
 RN SEQUENCE OF 30-503 FROM N.A.
 RC TISSUE=Brain;
 RA Anand R., Lindstrom J.;
 RL Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
 RN [9]
 RN SEQUENCE OF 6-493 FROM N.A.
 RC TISSUE=Epidermal Keratinocytes;
 RA Arredondo J., Grando S.A.;
 RT "Cloning cholinergic receptors in human keratinocytes.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=2;

CC Name=1;
 CC IsoId=P32297-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P32297-2; Sequence=VSP_000073;
 CC Note-No experimental confirmation available;
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC -----
 DR EMBL; M86383; AAC84176.1; -;
 DR EMBL; M37981; AAS59942.1; -;
 DR EMBL; U62432; AAB40110.1; -;
 DR EMBL; Y08418; CAA69695.1; -;
 DR EMBL; AJ007783; CAA07682.1; JOINED.
 DR EMBL; AJ007784; CAA07682.1; JOINED.
 DR EMBL; AJ007785; CAA07682.1; JOINED.
 DR EMBL; AJ007786; CAA07682.1; JOINED.
 DR EMBL; AJ007787; CAA07682.1; JOINED.
 DR EMBL; BC001642; AAH01642.1; -;
 DR EMBL; BC002996; AAH02996.1; -;
 DR EMBL; BC000513; AAH00513.1; -;
 DR EMBL; AF385584; AAK68110.1; -;
 DR EMBL; X53559; CAA37625.1; -;
 DR PIR; A37040; A37040.
 DR PIR; A53956; A53956.
 DR Genew; HGNC:1957; CHRNA3.
 DR MIM; 118503; -;
 DR GO; GO:0005892; C-nicotinic acetylcholine-gated receptor-chan.; TAS.
 DR GO; GO:0004889; F-nicotinic acetylcholine-activated cation-se.; TAS.
 DR GO; GO:0005215; F:transporter activity; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR GO; GO:0006832; P:small molecule transport; TAS.
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neu_chan_LBD.
 DR InterPro; IPR006201; Neu_chan.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR ION CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family; Alternative splicing; Polymorphism.
 FT SIGNAL 1 29 POTENTIAL.
 FT CHAIN 30 503 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-3 CHAIN.
 FT DOMAIN 30 238 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 239 263 POTENTIAL.
 FT TRANSMEM 271 289 POTENTIAL.
 FT TRANSMEM 305 326 POTENTIAL.
 FT DOMAIN 327 475 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 476 495 POTENTIAL.
 FT DISULFID 157 171 BY SIMILARITY.
 FT DISULFID 221 222 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 1 5 MALAV -> MGSGL (in isoform 2).
 FT VARSPLIC 1 5 /FTIG-VSP_000073.
 FT VARIANT 21 21 L -> LL.
 FT VARIANT 21 21 /FTIG-VAR_013240.
 FT CONFLICT 5 13 VSLPLALSP -> ALAAGAVA (IN REF. 2).
 FT CONFLICT 11 14 LSPP -> CRA (IN REF. 1).
 FT CONFLICT 100 100 D -> G (IN REF. 1).
 FT CONFLICT 132 133 DD -> TT (IN REF. 1).
 FT CONFLICT 235 235 I -> S (IN REF. 1).
 FT CONFLICT 430 430 L -> V (IN REF. 1).
 FT SEQUENCE 503 AA; 57309 MW; 8A9BEC5D71AEC7D6 CRC64;

Query Match 36.0%, Score 960; DB 1; Length 503;
 Best Local Similarity 41.0%; Pred. No. 7.9e-74;
 Matches 203; Conservative 90; Mismatches 172; Indels 30; Gaps 10;

QY 12 APAGLLLLCLLWPRGARGCYHEKRLHLLDHYNVLPVNVNEDSLPQLSFGTLMOII 71
 DB 12 SPRLLLLSLLP-VARASAEHLRFLERFEDNEIRPVANVSDPVIHFVEVSQV 70
 QY 72 DVDEKNOLLITNIWKLWMDNMLRWNTSDFGGVKDLRVPPHRLWKPDVLMYNSADEGFD 131
 DB 71 KVDEVNQIMETNLWLKQIWNQYKLNWPSDYGAEEFMRVPAQIKWPDIVLYNNAVGDFQ 130
 QY 132 STYPTNVVRNNGSLYVPPGIFKSTCKIDITWPEDDQRCMKFGSWTYDGYQLDLQLQ 191
 DB 131 VDDTKALKYTGVTWIPPAIFKSSCKIDITYFPDYQNTKMGFSWYDKAKIDLVL 190
 QY 192 DEGGDISSFVTNGEWELIGVGRNEIYNCCPEPYIDITFAVVIKRTLYFFNLIVP 251
 DB 191 G-SMNLDKDYWESEGAIIKAPGYKHDIKYNCCIEYDITISYIRKPLFYTNILIP 249
 QY 252 CVLIASMALGFTLPDPSGKSLGVTILLSLTVFLNMVAETPATSDAVPLLGTYFNCI 311
 DB 250 CLLISFLTVLVFLPSDGERKVTLCISVLLSLTVFLLVITETIPSTSLVPLICEYLLFT 309
 QY 312 MFWASSVSVTILNLNTHRHADTHMSDWTIRCFLVLPWLVRMSRP----GSATPPPP 367
 DB 310 MIFVTLISIVTVFVNLVHYRTPTTHMPSWYKTVFLNLLPRVMTPTNRSNEGNAQKPRP 369
 QY 368 ARVPPPPDLRLERS-SKSLLANVLIDDDFRHPQAOQPOC--CRYVRGGEEN-GAGLA- 422
 DB 370 LYGAELSNLWCFSAESKCGKEG-----YP-CQDGMCGYCHHRIKISNFSANLTR 419
 QY 423 AHSFCGVDYELSL-----ILKEIRVITDOMRKDEDEDADISDMKFAAMVVDRLCLI 473
 DB 420 SSSSESVAVLSLSALSPEIKAEIQSVKYIAENKAQNEAKEIQDDWNVYAMVIDRFLW 479
 QY 474 IFTLFTIATLAVLL 488
 DB 480 VFTLVCLGLTAGLFL 494

RESULT 10
 ACH2_HUMAN
 ID ACH2_HUMAN STANDARD; PRT; 529 AA.
 AC Q15822; Q9HAQ3;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
 GN CHRNA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=97062879; PubMed=8906617;
 RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
 RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
 RT Comparative structure of human neuronal alpha 2-alpha 7 and beta
 RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
 RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
 RT beta 4 subunits.;
 RL J. Mol. Neurosci. 7:217-228(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Groot Kormelink P.J.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Blechschmidt K., Rosenthal A.;

Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 MEMBRANE.
 -1- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
 OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-2 SUBUNIT CAN BE
 COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
 -1- SUBCELLULAR LOCATION: Integral membrane protein.
 -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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 or send an email to license@isb-sib.ch).

 EMBL; U62431; ABA0109.1; -;
 EMBL; Y16281; CAA76154.1; -;
 EMBL; AF311103; -; NOT_ANNOTATED_CDS.
 Genew; HGNC:1956; CHRNA2.
 MIM; 118502; -;
 GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. . .; TAS.
 GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . .; TAS.
 GO; GO:0007165; P:signal transduction; TAS.
 GO; GO:0007268; P:synaptic transmission; TAS.
 InterPro; IPR006029; Neur_chan_memb.
 InterPro; IPR006202; Neur_chan_LBD.
 InterPro; IPR006201; Neur_chan_LBD.
 Pfam; PF02931; Neur_chan_LBD; 1.
 Pfam; PF02932; Neur_chan_memb; 1.
 PRINTS; PR00252; NRIONCHANNEL.
 TIGRFAMs; TIGR00860; LIC; 1.
 PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 Transmembrane; Multigene family.
 FT SIGNAL 1 26 POTENTIAL.
 FT CHAIN 27 529 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 ALPHA-2 CHAIN.
 FT DOMAIN 27 264 EXTRACELLULAR.
 FT TRANSMEM 265 289 POTENTIAL.
 FT TRANSMEM 297 315 POTENTIAL.
 FT TRANSMEM 331 352 POTENTIAL.
 FT DOMAIN 353 502 CYTOPLASMIC.
 FT TRANSMEM 503 521 POTENTIAL.
 FT DISULFID 183 197 BY SIMILARITY.
 FT DISULFID 247 248 ASSOCIATED WITH RECEPTOR ACTIVATION
 (BY SIMILARITY).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 125 125 A -> T (IN REF. 3).
 SQ SEQUENCE 529 AA; 59735 MW; 7F512B06CCD9A9FD CRC64;
 Query Match 36.0%; Score 960; DB 1; Length 529;
 Best Local Similarity 38.9%; Pred. No. 8.4e-74;
 Matches 199; Conservative 90; Mismatches 171; Indels 52; Gaps 8;

QY 4 RARSHLAAPAGLLLLCLLWPRGARGCYHEKRLHLLDHYNVLPVNVNEDSLPQLSFG 63
 DB 35 RAPGDPLSSPSPTAL-----PQGSHTETEDRLFKHLFRGNRWARPVPNTSDVVIVRF 88
 QY 64 GLTLMQIIDVDKKNOLLITNIWKLWMDNMLRWNTSDFGGVKDLRVPPHRLWKPDVLMY 123
 DB 89 GLSLAQILIDVDKKNOMTTNWLKQWSDYKLRWNPADFGNITSLRVPSEMIWIDIVLY 148
 QY 124 NSADEGFDSTYPTNVVRNNGSLYVPPGIFKSTCKIDITWPEDDQRCMKFGSWTYD 183
 DB 149 NNADGEFAVTHMTKAHLFTSTGVVHVPPIAYIKSSCSIDVTFPFDDQCKMKFGSWTYDK 208
 QY 184 YQLDLQDEGGGDISSPVTNGEWELIGVGRNEIYNCCPEPYIDITFAVVIKRTLY 243

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Db 209 AKIDLE-QMEQTVLDKDYWESGEMAIIVNATGYNSKKYDCCAEIYPDVTFYAFVIRRLPLF 267
QY 244 YFENLIVPCVLIASMALLGFTLPDSGKLSGLVTLISLTVFLANVAETMATSDAVPL 303
Db 268 YINLIIPCLLSCTLVLYIPSCGCKITLCISVLLSLTVFLLLITIIIPSTSLVPL 327
QY 304 LGTYFNCIMFVASSVSTILINHHHADTHMSDWIRCVFLYWLPMVLRMSRPGSAT 363
Db 328 IGEYLLFTMIFVTLSTIVITFVLNVHRSPTHTPMHVYRGALLGCVPRWLLMRP--- 383
QY 364 TTPPARVPPPPLELRSSKSLANVLD-----IDDFR----- 398
Db 384 -PPVELCHP--LRLLKSPSYHWLESNDVAEREYVVEEDRWACAGHVAPSVGTLCSHG 440
QY 399 --HPQAOPOCCRYRYRGENGAGLAHSCFGVGYDLSLILKEIRVITDQMKEDADADI 456
Db 441 HLHSGASGPKAALLQEGE---LLSPH-----MOKALEGVHYIADHLRSEDADSSV 489
QY 457 SRDWKFAAMVDRLCLIIITFTIATLAVLL 488
Db 490 KEDWKYAMVIDRIELWLFIIVCFGLTGIGLFL 521
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RESULT 11

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ACH2_CHICK STANDARD; PRT; 528 AA.
AC P09480;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
OS Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88283624; PubMed=3267226;
RA Nef P., Onysier C., Alliod C., Couturier S., Ballivet M.;
RT "Genes expressed in the brain define three distinct neuronal
nicotinic acetylcholine receptors.";
RL EMBO J. 7:595-601(1988).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
MEMBRANE.
CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (ALSO CALLED BETA). A
FUNCTIONAL RECEPTOR SEEMS TO CONSIST OF TWO ALPHA-CHAINS AND
THREE NON-ALPHA CHAINS.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PRO0232; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 23
FT CHAIN 24 528
FT DOMAIN 24 239
FT TRANSMEM 240 264
FT TRANSMEM 272 290
FT TRANSMEM 306 327
FT TRANSMEM 328 501
FT TRANSMEM 502 520
FT DOMAIN 394 410
FT DISULFID 158 172
FT DISULFID 222 223
FT CARBOHYD 54 54
FT CARBOHYD 104 104
FT SEQUENCE 528 AA; 60675 MW; E76C6360AF876364 CRC64;
SQ
Query Match 36.0%; Score 959; DB 1; Length 528;
Best Local Similarity 39.2%; Pred No. 1e-73;
Matches 198; Conservative 84; Mismatches 161; Indels 62; Gaps 10;
QY 31 GYHEKRLHLHDHYNVLRPVVNESDPLQLSFGTLTLMQIIDVDEKNQLLTINWLKLEW 90
Db 31 GFAEDRLFKHLFTGYNRWSRPVNTSDVVIVKFGLSIAQLIDVDEKNQMTTNVLVKQEM 90
QY 91 NDMNLRWYTSDEGKYDLRVPPHRLWKPDVLMYNSADEGSDFTYPTNVVVRNNGSLYVP 150
Db 91 SDYKLWNPEDFDNVTISRVSEMIWIPDIVLYNNADGEFAVTHMTKAHLFSGKVKWVP 150
QY 151 PGIFKSTCKIDITWFPDDORCEMRFGSWTYDGYOLDLQDEGGDISFSVTNGEWELI 210
Db 151 PAIYKSSCSIDVTYFFDQONCKMFGSWTYDKAKIDLE-NMEHVDLKDYWESEWAIL 209
QY 211 GVPGRKRIYVNCPEPYIDITFAVIRKRLTYFNFNLIVPCVLIASMALLGFTLPDSG 270
Db 210 NAIGRYNSKKYDCCTEIPDITFYEVIRRLPFLYINLIIPCLLSCTLVFLVLPDSCG 269
QY 271 EKLSLGVTLISLTVFLANVAETMATSDAVPLLTGYFNCIMFVASSVSTILINLNVH 330
Db 270 EKITLCISVLLSLTVFLLLITIIIPSTSLVPLIGEYLLTFMIFVTLSTIIITFVLNVH 329
QY 331 RHADTHEMSDWIRCVFLYWLPMVLRMSRPGSATTPPARVP-----PPDLELRERS 382
Db 330 RSPSTHTPMHVRSFELGFIPLWLFMKR-----PPLLLPAEGTGGYDPPGTRL--ST 380
QY 383 SKSLANVLDIDDDFRHPQAQPOQ-----CCRYRYRGENGAGLAH--SC---- 426
Db 381 SRCWLET--DVDDKWEKEEEEEEEEEEEKAYPSRVPSGSGQ---GTOCHYSCERA 435
QY 427 -----FGVDYELSL-----ILKEIRVITDQMKEDADADISRWKFA 463
Db 436 SKASGGAPQVPLKGEVSGSQGLTSPSLRALEGVQVIADHLRAEDADFVSKEDWKYV 495
QY 464 AMVVDRLCLIIITFTIATLAVLL 488
Db 496 AMVIDRIELWFIIVCLLTGTVGLFL 520
RESULT 12
ID ACH1_DROME STANDARD; PRT; 567 AA.
AC P09478; O9VC74;
DT 01-MAR-1989 (Rel. 10, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
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QY 310 C1MFVWASSVSTILINLTHHRRADTHEMSDNRVCLVWLPVLRMSRPGSATPPPAR 369
 Db 309 FTMLVTLVSVVTVIADVNFSPVTHRMVQVRLFIQILPKLLCIERP--KKEEPED 366
 QY 370 VPP-----PPDL-LRERSKSL-----L 387
 Db 367 QPPEVLTUVYHLPDPVVKVNTDSKRFSDYGIPLPASHRFDLAAGISAHCFAPPL 426
 QY 388 ANVLDT--DDFRHPQAQ---QPQCCRYRGGENGAGLAHS-----CFGVYD--ELS 434
 Db 427 PSSLPPLGADDDLFPSGLNGDISPGCC-----PAAAAAADLSTFEKPYAREME 478
 QY 435 LILKETRVTDQMRKDDADISRWKFAAMVVDRLCLIFLTFTIATVALLSAPHI 493
 Db 479 KTIQGRFTAQHVKNKDFESVEDWKYVAMVLDRLMFLWIFATACVVGFTALILQAPSL 537

RESULT 13
 ACH2_RAT
 ID ACH2_RAT STANDARD; PRT; 511 AA.
 AC P12389; 008952;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
 GN CHRNA2 OR ACRA2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=88178113; PubMed=2832952;
 RA Wada K., Ballivet M., Boulter J., Connolly J.G., Wada E.,
 RA Deneris E.S., Swanson L.W., Heinemann S.F., Patrick J.;
 RT "Functional expression of a new pharmacological subtype of brain
 RT nicotinic acetylcholine receptor.";
 RL Science 240:330-334(1988).
 RN [2]
 RP REVISIONS.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RA Boulter J.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-2 SUBUNIT CAN BE
 CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC
 CC EMBL; L10077; AAB60900.1; -;
 CC EMBL; M20297; AAA40664.1; -;
 CC EMBL; M20292; AAA40664.1; JOINED.
 CC EMBL; M20293; AAA40664.1; JOINED.
 CC EMBL; M20294; AAA40664.1; JOINED.
 CC EMBL; M20295; AAA40664.1; JOINED.
 CC EMBL; M20296; AAA40664.1; JOINED.
 CC PIR; A40110; A40110.
 CC InterPro; IPR006029; Neu_channel_memb.
 CC InterPro; IPR006202; Neur_chan_LBD.
 CC InterPro; IPR006201; Neur_channel.

DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRfams; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 27
 FT CHAIN 28 511
 FT DOMAIN 28 241
 FT TRANSMEM 242 266
 FT TRANSMEM 274 292
 FT TRANSMEM 308 329
 FT DOMAIN 330 484
 FT TRANSMEM 485 503
 FT DOMAIN 391 402
 FT DISULFID 160 174
 FT DISULFID 224 225
 FT CARBOHYD 56 56
 FT CARBOHYD 106 106
 FT CARBOHYD 212 212
 FT CONFLICT 494 494
 FT SEQUENCE 511 AA; 58611 MW; 3824E83BB01D613B CRC64;
 SQ
 Query Match 35.7%; Score 951; DB 1; Length 511;
 Best Local Similarity 39.4%; Pred. No. 4.7e-73;
 Matches 198; Conservative 90; Mismatches 167; Indels 48; Gaps 8;
 QY 16 LLLLCLLMWRGARGCYHEKRLHLLHLLDHYNLERPVNVEDPLQSLFGLTLMQIIDVDE 75
 Db 19 LLLVPAVLVTQGSHT-HAEDRLFKLFGGYNWRAPVPTSDVIVRFGLSIAQLIDVDE 77
 QY 76 KNOLLITNLWLKLEWDMNLKNTSDFGCVKDLRYPHPHLKLPDVLWYNSAGDEGDSYTP 135
 Db 78 KNQMTNVNLKQEWNDYKLRWDPAEFGNVTSLRVPSEMIWIPDIVLYNNADGEFAVTHM 137
 QY 136 TNVYVRNNGSLYVPPGIFKSTCKIDITWFPDDQRCENKFGSWTYDGYQLDLQDEGG 195
 Db 138 TRAHLLFTGTVHWVPPAIYKSSCIDVTFPFDOQCKMKFGSWTYDKAKIDLE-QMERT 196
 QY 196 GDISSFVNGEWELIGVPGKREIYNYNCCPEYIDITFAVIRRKTYLYFFNLIVPCVLI 255
 Db 197 VDLKDYWESEWAIINATGYNKRYDCAEIPDVITYFVIRRLPLFTINLIIPCLLI 256
 QY 256 ASMALGFTLPDPSGEKLSGLVTILLSLTFVLMVAETMPATSDAVPLGLTYFNCIMRW 315
 Db 257 SCLTVLVFVLPSECEKITCLISVLSLTVLILLTEIIPSTSLVPLIGEYLLFTMIFV 316
 QY 316 ASSVYSTILILNHHRHADTHEMSDNRVCLVWLPVLRMSRPGSATPPPARVPPPD 375
 Db 317 TLSIVITVFLVNVHRRSPSTHNNMNVRVALLGRVPRWLMNRP-----LPPMELHGS 371
 QY 376 LELRRSSKSLANVLDDDDPRHPQAQCCRYRGGENG-----GAGLAHSCFGVDY- 431
 Db 372 LKL--SPSYHWLETNDAGERETEETEEEE-----DENICVAGL-PDSSMGVLVG 420
 QY 432 -----ELSLILKEIRVITDQMRKDDADISRWKFAAM 465
 Db 421 HGGLHLRAMEPTKTPSQASEILLSPQIQKALEGVHYIADRLSEDDSSKVEDKRYVAM 480
 QY 466 VVDRCLLIIFTLTITATLAVLL 488
 Db 481 VVDRIFLWFLIIVCFLTIGLFL 503
 RESULT 14
 ID ACH3_BOVIN
 AC Q07263;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)
 Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
 GN CHRNA3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92319195; PubMed=1620271;
 RA Criado M., Alamo L., Navarro A.;
 RT "Primary structure of an agonist binding subunit of the nicotinic
 FT acetylcholine receptor from bovine adrenal chromaffin cells.";
 RL Neurochem. Res. 17:281-287(1992).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR ALL SUBUNITS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT
 CC TYPE OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X57032; CAA40348.1; .
 DR PIR; S60589; S60589.
 DR InterPro; IPR006029; Neu_channel_memb.
 DR InterPro; IPR006020; Neur_chan_LED.
 DR InterPro; IPR006201; Neur_channel.
 DR Pfam; PF02931; Neur_chan_LED; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFAMS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 DR Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 21
 FT CHAIN 22 495
 FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT ALPHA-3 CHAIN.
 FT DOMAIN 22 230
 FT TRANSMEM 231 255
 FT TRANSMEM 263 281
 FT TRANSMEM 296 318
 FT TRANSMEM 319 467
 FT TRANSMEM 468 487
 FT DISULFID 149 163
 FT DISULFID 213 214
 FT ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 45 45
 FT CARBOHYD 162 162
 FT N-LINKED (GLCNAC. .) (POTENTIAL).
 FT SEQUENCE 495 AA; 56914 MW; 322825629821EA07 CRC64;
 Query Match 35.1%; Score 936.5; DB 1; Length 495;
 Best Local Similarity 39.5%; Pred. No. 7.7e-72;
 Matches 198; Conservative 89; Mismatches 181; Indels 33; Gaps 9;
 OY 5 ARRSLAPAGLLLLLCLLMPRGARCGVHEKRLHLLHDHYNLVLPVWNSDPLQLSFG 64
 DB 2 ARRSRLR-----LILLLLLP-VASTDAERHLERLEFEDYNEIRPVANVSDPVIQFE 55
 OY 65 LFLMQIIDVDEKNOILLITNWKLEWMDNMLRWNTSDFGVKDLRPPHRLKWDPLVMYN 124
 DB 56 VMSQLVKVDEVNOIMETNMLKQIWDYKLNWPSDYDGAEEFMVPAEKIKWDPLVYN 115
 OY 125 SADEGFSDTYPTNVVNRNNGSLVYPGCFKSTCKIDITWFPDDQRCMKFGSWTYDGY 184

Db 116 NAVGDFQVDDKTKALLKTYTGEVTPWIPPAIFKSSCKIDVTYFPFYQNTMKFGSWSYDKA 175
 OY 185 QLDLQLODEGGDISFSFTNGEWELIGVPGKRNIYYNCCPEPIDITFAVVIKRTLYY 244
 Db 176 KIDLVLIG-SSMNLKDYWESGEWAIKAPGYKHDIKYNCCIEIYDPITYSLYIRLPLFY 234
 OY 245 FNNLIVPCVLIASMALLGFTLPDGSGBKLSGVITILLSVFLNMVAETMPATSDAVPLL 304
 Db 235 TINLIIPCLLISFLTVLVFLVLPSCGKEKVTLCISVLLSLTVFLVAVITETIPSTSLVPLI 294
 OY 305 GTFNCIMFWVASSVSTILLNLYHHRHADTHEMSDWIRCVFLYWLFWLMSRP-----G 360
 Db 295 GEXLLFTMIETVLSIVITVFLNVHYRTPTHTTPAWVKTFILNLLPRVFMFTRPASNEG 354
 OY 361 SATTPPPARVPPDPDLRERSKSLANVLDDDFRHFQAOQPOC--CRYYRGGEN- 417
 Db 355 NTQPRPFYSAELSNLNCFSRIESKVKCEGYPQDGL-----CGYCHHRAKISNF 405
 OY 418 GAGLA-AHSCFGVDYELSL-----ILKEIRVITDQMRKDDDEDADISRDWKAFAVV 467
 Db 406 SANLTSSSESVDVLSLSALSPEIKAEIQSVKYIAENKMAQNEAKEIQDDWKYVAMVI 465
 OY 468 DRICLIITFTTIATLAVLL 488
 Db 466 DRIFLWVFIILVILGTAGLFL 486
 RESULT 15
 ACH3_RAT
 ID ACH3_RAT STANDARD; PRT; 499 AA.
 AC P04757;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
 GN CHRNA3 OR ACRA3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86118671; PubMed=3753746;
 RA Boulter J., Evans K., Goldman D.J., Martin G., Treco D.,
 RA Heinemann S.F.,
 RA Patrick J.;
 RT "Isolation of a cDNA clone coding for a possible neural nicotinic
 RT acetylcholine receptor alpha-subunit.";
 RL Nature 319:368-374(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88041184; PubMed=2444984;
 RA Boulter J., Connolly J.G., Deneris E.S., Goldman D.J., Heinemann S.F.,
 RA Patrick J.;
 RT "Functional expression of two neuronal nicotinic acetylcholine
 RT receptors from cDNA clones identifies a gene family.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7763-7767(1987).
 RN [3]
 RP SEQUENCE OF 1-21 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=94193711; PubMed=8144606;
 RA Yang X., McDonough J., Fyodorov D., Morris M., Wang F.,
 RA Deneris E.S.;
 RT "Characterization of an acetylcholine receptor alpha 3 gene promoter
 RT and its activation by the Pou domain factor SCIP/Tst-1.";
 RL J. Biol. Chem. 269:10252-10264(1994).
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-3 SUBUNIT CAN BE

CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
CC -I- SUBCELLULAR LOCATION: Integral membrane protein.
CC -I- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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CC -----
DR EMBL; X03440; CAA27170.1; -
DR EMBL; L31621; AAA1673.1; -
DR EMBL; U04961; AAA18001.1; -
DR InterPro; IPR006029; Neu_chan_memb.
DR InterPro; IPR006202; Neu_chan_LBD.
DR InterPro; IPR006201; Neu_chan.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 499 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT ALPHA-3 CHAIN.
FT EXTRACELLULAR.
FT DOMAIN 26 234
FT TRANSMEM 235 259
FT TRANSMEM 267 285
FT TRANSMEM 301 322
FT DOMAIN 323 471
FT TRANSMEM 472 491
FT DISULFID 153 167
FT DISULFID 217 218
FT CARBOHYD 49 49
FT CARBOHYD 166 166 N-LINKED (GLCNAC. .) (POTENTIAL).
FT SEQUENCE 499 AA; 56997 MW; D66C491E832B9C34 CRC64;
Query Match 34.9%; Score 930; DB 1; Length 499;
Best Local Similarity 39.0%; Pred. No. 2.8e-71;
Matches 194; Conservative 92; Mismatches 181; Indels 30; Gaps 9;
QY 10 LAAPAGLLLCILPRGARGCYHEKRLHLLHDYVNLVLPVWVESDPLQLSFGLTLMQ 69
DB 6 LPPPLSLMLVLMPLP-AASASEAHRLEFQYLFEDYNEIRPVANVSHPVIIQFEVMSQ 64
QY 70 IIDVDEKNOLLITNIWLKLEWDMNLNRWNTSDFGVKDLRVPVPHRLWKPDVLMYNSADEG 129
DB 65 LVKVDENVQIMETNLWLKQIWDYKLWKKPSDYQGVFEFMRVPAEKIWKPDIVLYNNADGD 124
QY 130 FDSYPTNVVVRNNGSLVPGIFKSTCKIDITWFPDDQRCMKFGSWYDGYQLDLQ 189
DB 125 FQVDDKTKALLYGEVTWIPFAIFKSKCKIDVTYFPDYQNCYQCTMKFGSWYDGYQLDLV 184
QY 190 LQDEGGDITSSFTNGEWELIGVPGKRNEIYCCPEPYDITFAVIRKTYLYFFNLI 249
DB 185 LIG-SSMNLKDWESGEWAIKAPGYKHEIKYNCCEEIYQDITYSLYIRRLPLFTINLI 243
QY 250 VPCVLIASMALLGFTLPDPSGKLSLGVITLLSLTVFLNMVAETMPATSDAVPLLGTYFN 309
DB 244 IFCLLISFTLVFLVLPSCGKVTLCISVLSLAVFLAVITETIPSTSLVIPLIGEYLL 303
QY 310 CIMFWVASSVSTILINLHHRADTHEMSDIRCVFLWLPWLRLMSRPSGAT-TPPPA 368
DB 304 FTMIFVTLISIVTVFLNVHYRTPTHTPTWVKAFLNLLPRVFMFTRPTSGEGDTPKT 363
QY 369 RYPPPPDLE- ---LRERSKSLLANVLIDDDHFRHQAQPOC- -CRYRGGEEN-GAGL 421
DB 364 RTFYGAELSNLNCFSRADSKCKEG- -----YP-CODGTCGYCHRRVRKISNFSANL 413

QY 422 -----AAHSCFGVDYELSLILKEIRVITDQMRKDDDEDADISRDWKFAMVVDRLC 471
DB 414 TRSSSSSESYNAVLSLSALSPEIKETQSVKYIAENKMAQNVAKEIQDDNKYVAMVIDRIF 473
QY 472 LIIFTLTITATLAVLL 488
DB 474 LWFVILVCLGTAGLFL 490

Search completed: August 13, 2003, 15:26:11
Job time : 11.386 secs

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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:45 ; Search time 18.5263 Seconds
(without alignments)
2574.698 Million cell updates/sec

Title: US-09-303-232-4
Perfect score: 2665
Sequence: 1 MGRARRSHLAAPAGLLLLL.....LFTIATLAVLSAPHIMVS 496
Scoring table: BLOSOM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1267	47.5	502	2 JN0113	nicotinic acetylch
2	1242	46.6	502	2 G02259	alpha 7 neuronal n
3	1241	46.6	502	1 ACHUA7	nicotinic acetylch
4	1241	46.6	502	2 A57175	nicotinic acetylch
5	1232.5	46.2	502	2 T01378	nicotinic receptor
6	1219.5	45.8	511	2 JH0173	alpha-bungarotoxin
7	1201	45.1	498	2 S68588	nicotinic acetylch
8	1141	42.8	461	2 T25671	hypothetical prote
9	1060	39.8	560	2 T19622	hypothetical prote
10	1055.5	39.6	542	2 T19862	hypothetical prote
11	979	36.7	557	2 S12359	nicotinic acetylch
12	962	36.1	503	2 A53956	nicotinic acetylch
13	959	36.0	528	1 ACCH2N	nicotinic acetylch
14	957.5	35.9	567	1 ACFFA1	nicotinic acetylch
15	954	35.8	502	2 A37040	nicotinic acetylch
16	953	35.8	511	2 A40110	nicotinic acetylch
17	936.5	35.1	495	2 S60589	acetylcholine rece
18	932	35.0	499	2 A24572	nicotinic acetylch
19	926	34.7	576	1 ACFFA2	nicotinic acetylch
20	918.5	34.5	456	1 ACCH4N	nicotinic acetylch
21	908.5	34.1	491	1 ACCHNN	nicotinic acetylch
22	904	33.9	622	1 ACCH4N	nicotinic acetylch
23	903.5	33.9	498	2 G02421	nicotinic acetylch
24	902.5	33.9	502	2 S10505	nicotinic acetylch
25	902	33.8	461	2 I50548	acetylcholine rece
26	901	33.8	503	2 JH0174	nicotinic acetylch
27	900.5	33.8	494	2 T02889	nicotinic acetylch
28	899	33.7	461	1 ACRYA1	nicotinic acetylch
29	898.5	33.7	512	2 B37014	nicotinic acetylch

ALIGNMENTS

RESULT 1

JN0113

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
N;Alternate names: alpha-bungarotoxin-binding protein alpha chain
C;Species: Gallus gallus (chicken)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
C;Accession: JN0113; JH0172; S28018; B25738; S26566
R;Couturier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.
Neuron 5, 847-856, 1990
A;Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is development
A;Reference number: JN0113; MUID:91097796; PMID:1702646
A;Accession: JN0113
A;Molecule type: DNA
A;Residues: 1-502 <CD>
A;Cross-references: GB:X69586; NID:g287756; PIDN:CAA48576.1; PID:g287757
A;Experimental source: white leghorn; brain
R;Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A;Title: Brain alpha-bungarotoxin binding protein cDNAs and MABS reveal subtypes of t
A;Reference number: JH0172; MUID:90315158; PMID:2369519
A;Accession: JH0172
A;Molecule type: mRNA
A;Residues: 1-502 <SCH>
A;Cross-references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078
A;Experimental source: brain
R;Matter-Sadinski, L.; Hernandez, M.C.; Rztocil, T.; Ballivet, M.; Matter, J.M.
EMBO J. 11, 4529-4538, 1992
A;Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter
A;Reference number: S28018; MUID:93049204; PMID:1425587
A;Accession: S28018
A;Molecule type: DNA
A;Residues: 1-18 <MAS>
A;Cross-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320
A;Experimental source: white leghorn; erythrocyte
R;Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.;
Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
A;Title: Brain and muscle nicotinic acetylcholine receptors are different but homolog
A;Reference number: A94055; MUID:85270494; PMID:3860855
A;Accession: B25738
A;Molecule type: protein
A;Residues: 24-25,'ET',28-41,'X',43-45,'X',47 <CON>
C;Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is locali
C;Genetics:
A;Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
C;Superfamily: acetylcholine receptor
C;Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprote
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr
F;231-254/Domain: transmembrane #status predicted <TR1>
F;262-280/Domain: transmembrane #status predicted <TR2>
F;296-317/Domain: transmembrane #status predicted <TR3>
F;470-488/Domain: transmembrane #status predicted <TR4>

nicotinic acetylch
nicotinic acetylch
nicotinic acetylch
nicotinic acetylch
nicotinic acetylch
nicotinic acetylch
acetylcholine rece
nicotinic acetylch
probable nicotinic
nicotinic acetylch
nicotinic acetylch
hypothetical prote
nicotinic acetylch
nicotinic acetylch
hypothetical prote

F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #status predicted
F:415/Binding site: phosphate (Thr) (covalent) #status predicted
F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 47.5%; Score 1267; DB 2; Length 502;
Best Local Similarity 48.6%; Pred. No. 1.9e-102;
Matches 249; Conservative 83; Mismatches 144; Indels 36; Gaps 6;

Qy 1 MGRARRSHLAAPAGLLLLCLLWPRGARGCYHEKRLLHLLDHNVLRYLERNVNESDPLQ 60
Db 1 MGLRALMLLLAAGLV-----RESLQGEFORKLYKELLKYNPLERPVANDSPLT 52

Qy 61 LSGGLTLMQIIDVDEKNOLLITNIWLKLEWDMNLRWNTSDFGVKDLRVPPHRLWKPDV 120
Db 53 VYFTLSLMQIMDVDEKNOLLITNIWLQWYDTHLQWNVSEYPGVKVNRFPDGLIWKPD 112

Qy 121 LMVNSADGFDSTPTNVVNRNGSCLYVPPGIFKSCICKIDITWFPDDQCEMKFGSWT 180
Db 113 LLYNSADRFDATEHTNVNNSGHCQYLPPIFKSSCYIDRVFPDFQVCKNLKFGSWT 172

Qy 181 YDGLQDLQDEGGDISFTVNGEWELIGVPGKRNEYIYNCCPEPIDITFAVIRRK 240
Db 173 YGWSLQDQGE---ADISGYSINGEWDLVGPKRTESFYECCKEYPDITFTVTHRR 229

Qy 241 TLYTFENLIVPCVLIASALLGFTLPDPSGKLSLGVITLLSVFLNMVAETMPATSDA 300
Db 230 TLYGLNLLIPCVLISALALLVFLLPADSGEKISLGITVLLSVFLNMVAEIMPATSDS 289

Qy 301 VPLLGTFVNCIMFVASSVSTILLINLHRRHADTHEMSDWIRCVFLYVLPVLRMSRPG 360
Db 290 VPLIAQFASPMIIVGLSVVTVIVLQVHHDPDGGKMPKWRVILLNMCAWFLRMKRP 349

Qy 361 SATTPPARVPPDLELRSSKSLANVLD-----IDDDFRHPQAAQ 404
Db 350 E-----DKVRPAQKHQRCSLSMEMNTVSGQCSNGNMLYIGFRLDGVHCTPTDS 403

Qy 405 PQCCRYRGK--ENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDEADISRWK 462
Db 404 GVICGRMTCSPTEENLHSGHPSEG-DPDLAKILEEVRYIANFRDQDEBEACNWK 462

Qy 463 AAMVVDRLCLIFLFTIATLAVLSAPHIM 494
Db 463 AASVVDRLCLMAFSVFTIICITIGILMSAPNEV 494

RESULT 2
G02259

alpha 7 neuronal nicotinic acetylcholine receptor - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 20-Aug-1999
C:Accession: G02259
R:Leonard, S.
submitted to the EMBL Data Library, November 1995
A:Reference number: H00936
A:Accession: G02259
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <LEO>
A:Cross-references: EMBL:U40583; NID:g1125076; PIDN:AAA83561.1; PID:g1125077
C:Superfamily: acetylcholine receptor

Query Match 46.6%; Score 1242; DB 2; Length 502;
Best Local Similarity 46.0%; Pred. No. 2.8e-100;
Matches 240; Conservative 84; Mismatches 128; Indels 70; Gaps 6;

Qy 12 APAGLLLLCLLWPRGARGCYHEKRLLHLLDHNVLRYLERNVNESDPLQISFGLTLQII 71
Db 4 SPGGVWLALASLLHVSLOGEFORKLYKELKYNPLERPVANDSPLTYVFSNLLQIM 63

Qy 72 DVDEKNOLLITNIWLKLEWDMNLRWNTSDFGVKDLRVPPHRLWKPDVLMVNSADGFD 131
Db 64 DVDEKNOLLITNIWLQWYDTHLQWNVSEYPGVKVNRFPDGLIYNLSADRF 123

Qy 132 STYPTNVVNRNGSCLYVPPGIFKSCICKIDITWFPDDQCEMKFGSWTYDGYOLDLQ 191
Db 124 ATPHTNLVNPSCGHCQYLPPIFKSSCYIDRVWFPDVQVHCKLKFSGSYSGWSLDLQ 183

Qy 192 DEGGDISFTVNGEWELIGVPGKRNEYIYNCCPEPIDITFAVIRKTLTYFENLIVP 251
Db 184 E---ADISGYSINGEWDLVGIPGRSERFYECCKEYPDVTFTVTHRRRTIYGLNLLIP 240

Qy 252 CVLIASALLGFTLPDPSGKLSLGVITLLSVFLNMVAETMPATSDAVPLLGYFNCI 311
Db 241 CVLISALALLVFLLPADSGEKISLGITVLLSVFLNMVAEIMPATSDSVPLIAQYFAST 300

Qy 312 MFVASSVSTILLINLHRRHADTHEMSDWIRCVFLYVLPVLRMSRPG----- 360
Db 301 MIIVGLSVVTVIVLQVHHDPDGGKMPKWRVILLNMCAWFLRMKRPDGVKVPACQHK 360

Qy 361 -----SATTPPAR-----VPPDLELRSSKSLANVLD 392
Db 361 QRRCSLASEMSAVAPPSPASNGNMLYIGFRLDGVHCVPTPDGSGVCGMACSPH----- 416

Qy 393 IDDDFRHPQAAQPOCCRYRGGEENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDE 452
Db 417 -DEHLH-----GGQPPEG-----DPDLAKILEEVRYIANFRCODE 452

Qy 453 DADISRWKFAAMVVDRLCLIFLFTIATLAVLSAPHIM 494
Db 453 SEAVCSEWKFACVVDRLCLMAFSVFTIICITIGILMSAPNEV 494

RESULT 3
ACHUA7

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1996 #sequence_revision 31-Jan-1997 #text_change 22-Jun-1999
C:Accession: I37185; A54194; S60309
R:Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.
Mol. Pharmacol. 45, 546-554, 1994
A:Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from th
omers expressed in Xenopus oocytes.
A:Reference number: I37185; MUID:94195283; PMID:8145738
A:Accession: I37185
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <PEN>
A:Cross-references: EMBL:X70297; NID:g496606; PIDN:CAA49778.1; PID:g496607
A:Experimental source: brain neuroblastoma cell line SHSY-5Y
R:Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzaretti, M.; Heinemann, S.
Genomics 19, 379-381, 1994
A:Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotini
A:Reference number: A54194; MUID:94245214; PMID:8188270
A:Accession: A54194
A:Molecule type: mRNA
A:Residues: 24-363, 'S', 365-374, 'A', 376-408, 'AWPAP', 414-502 <CHI>
A:Cross-references: GB:Z23141; NID:g457736; PIDN:CAA80672.1; PID:g457737
A:Experimental source: retina
C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is locali
C:Genetics:
A:Gene: GDB:CHRNA7
A:Cross-references: GDB:I38751; OMIM:118511
A:Map position: 15q14-15q14
A:Note: defects in this gene have been associated with mental retardation and schizop
C:Complex: the functional receptor molecule is a heteropentamer with two alpha chains
C:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter recept
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr
F:231-254/Domain: transmembrane #status predicted <TR1>
F:262-280/Domain: transmembrane #status predicted <TR2>
F:296-317/Domain: transmembrane #status predicted <TR3>
F:470-488/Domain: transmembrane #status predicted <TR4>
F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted


```

Db      114  LYNSEADREFDTHNVLNVSAGHCQYLPDGFKSSCIDVRWFPDVOQCKLFGWSY 173
QY      182  DGYQLDLQDGGDISFVTNGEWELGYPGRKRNEIYVNCPEPYIDITFAVYIRKKT 241
Db      174  GWSLSDLQMQE---ADISSYIPNGEWDLMGIPGRKNEKFECCKEPYDVITYVTMRRT 230
QY      242  LYEFNLIVPCVLTASMAALLGFTLPDPSGEKLSGVTTLLSLTVFLNVAETMPATSDAV 301
Db      231  LYGLNLILPCVLISALALLVFLPADSGEKISLGTIVLLSLTVFLLVAETMPATSDSV 290
QY      302  PLIGTYFNCIMFVASSVSTILILNYHHRHADTHEMSDWIRCVFLYWLWPLVLRMRSPGS 361
Db      291  PLIAQYFASFTMIIVGLSVVTVIVLYHHHDGDKGPKWTRILLNNCAWFLMRKRGPE 350
QY      362  ATTPTTPPARVPP-----PPDLERRSKSLANVLIDIDDDF-----H 399
Db      351  DKVRPACQKPRRCSLASVELSAGAPPTS-----GNLLYI---GFGLEGHICA 398
QY      400  POAQOQCCRYRGEENGAGL--AAHSCFGVDVLSILKEIRVITDOMRKDDADIS 457
Db      399  PTPDSGVVCGRLACSPTHDEHLHGHPSDG-DPDLAKILEEVRYIANRRCQDESEVIC 457
QY      458  RDMKFAAMVDRLCLIIITFTIATLAVLSAPHIM 494
Db      458  SEWFAACVDPCLMAFVSFTIICIGILMSAPNFV 494

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RESULT 6

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JH0173
alpha-bungarotoxin-binding protein alpha-2 chain precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999
C:Accession: JH0173
R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MAbS reveal subtypes of this
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0173
A:Molecule type: mRNA
A:Residues: 1-511 <SCH>
A:Cross-references: GB:X52296; NID:g63081; PIDN:CAA36544.1; PID:g63082
A:Experimental source: brain
A:Note: this sequence is similar to acetylcholine receptor alpha chains
C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudodend
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <AE
F:239-262/Domain: transmembrane #status predicted <TM1>
F:270-288/Domain: transmembrane #status predicted <TM2>
F:304-323/Domain: transmembrane #status predicted <TM3>
F:479-496/Domain: transmembrane #status predicted <TM4>
F:54/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match      45.8%; Score 1219.5; DB 2; Length 511;
Best Local Similarity 46.3%; Pred. No. 2.7e-98;
Matches 236; Conservative 88; Mismatches 131; Indels 55; Gaps 9;

```

```

QY      20  LCLLWP-----RGARGYHEKRLHLLDHYNVLPRPVNESDPLQLSLGLTLMOLID 72
Db      14  LC-LWASLFLFFKVSQGESQRRLYRDLNRLNKLPRVWNSQPIVVELQLSLQLIID 72
QY      73  VDEKNQLLITNLKLEWDMNLRWNTSDFGVKDLRVPPHRLMKPDVIMYNSADEGFDPS 132
Db      73  VDERNOVLITNAWLQMYVWDIYLSWDQYEGVGNLRFPSPQINVPDILLYNSADERDA 132
QY      133  TYPNVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCMKGSGWTYDGYQLDLQD 192
Db      133  TFHNVNLVYSGSQYIPPGILKSTCYIDVRVFPDVKCDLKFSGSWTHSGWLIDLQMLE 192
QY      193  EGGDGLSISFVTNGEWELGYPGRKRNEIYVNCPEPYIDITFAVYIRKKTLYEENLIVPC 252

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Db      193  ---ADISNYISNGEWDLVGVCKRNLLEYECKEPEYPDVITYITMRRTLYLGLNLLIPC 249
QY      253  VLIASMAALLGFTLPDPSGEKLSGVTTLLSLTVFLNVAETMPATSDAVPLLGTYFNCIM 312
Db      250  VLISGLALLVFLPADSGEKISLGTIVLLSLTVFLLVAETMPATSDSVPLLIAQYFASIM 309
QY      313  FWASSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLWPLVLRMRSPGSATTPPARVPP 372
Db      310  VIVGLSVVTVIVLQFHHDHPQAGKMPRWVRVILLNNCAWFLMRKKGPKGENTKPLSKYSY 369
QY      373  PPDLERRSKSLANVLIDIDDDFRHPQAQPOQ-----CRRYRGEENG 418
Db      370  PK-----HPSLKNTEMNVL-----PGHQPSNGNMIYSHYHTMENFCCPO---NNDLG 413
QY      419  AGLAHSC-FGVDEY-----LSLILKEIRVITDOMRKDDADISRDWKFAA 464
Db      414  SKSGKITCPLSEDNEHVQKALKALMDITPVIIVKILEEVQFIAMFRFRKQDEGEICSEWKFAA 473
QY      465  MVDRCLLIITFTIATLAVLSAPHIM 494
Db      474  AVIDRLCLVAFTFAIICITFTILMSAPNFI 503

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RESULT 7

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S68588
nicotinic acetylcholine receptor alpha-1 chain precursor (clone Ce21) - Caenorhabdit
C:Species: Caenorhabditis elegans
C:Date: 06-Dec-1996 #sequence_revision 07-Feb-1997 #text_change 20-Aug-1999
C:Accession: S68588; S57496
R:Ballivet, M.; Alliod, C.; Bertrand, S.; Bertrand, D.
J. Mol. Biol. 258, 261-269, 1996
A:Title: Nicotinic acetylcholine receptors in the nematode Caenorhabditis elegans.
A:Reference number: S68587; MUID:96196478; PMID:8627624
A:Accession: S68588
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-498 <BAL>
A:Cross-references: EMBL:X83887; NID:g872087; PIDN:CAA58764.1; PID:g872088
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-498/Product: nicotinic acetylcholine receptor alpha-1 chain #status predicted <M

```

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Query Match      45.1%; Score 1201; DB 2; Length 498;
Best Local Similarity 46.0%; Pred. No. 1.1e-96;
Matches 230; Conservative 89; Mismatches 151; Indels 30; Gaps 7;

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```

QY      17  LLLCLLWPRGARGYHEKRLHLLDHYNVLPRPVNESDPLQLSLGLTLMOLIDVDEK 76
Db      6  LLISCAILAAPTLSGLQERRLYEDLMRYNNLRLPRVANHSEPTVHLKVALQOIIDVDEK 65
QY      77  NQLLITNLKLEWDMNLRWNTSDFGVKDLRVPPHRLMKPDVIMYNSADEGFDSTYPT 136
Db      66  NOVYVNAWLDYTWNDYLNVDKAEYGNITDVRFPAGKIWKPDVLLYNSVDNFDSTYQT 125
QY      137  NVVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCMKGSGWTYDGYQLDLQDEGG 196
Db      126  NMIVYSTGLVHWVPPGIFKSTCKIDIQWFFDEQRCFFKFGSWTYDGYQLDLQ-PATG 184
QY      197  DISFVTNGEWELGYPGRKRNEIYVNCPEPYIDITFAVYIRKKTLYEENLIVPCVLIA 256
Db      185  DISEYISNGEWALPTTVVERNEKFDCCPEPDVHFYLMHMRRTLYYGFNLIMPCILIT 244
QY      257  SMALLGFTLPDPSGEKLSGVTTLLSLTVFLNVAETMPATSDAVPLLGTYFNCIMFWA 316
Db      245  LMTLLGFTLPDAGEKITIQTIVLLSICFELSIYSEMSPTSEAVPLLGIPTCCMIVT 304
QY      317  SSVVSTILILNYHHRHADTHEMSDWIRCVFLYWLWPLVLRMRSPGS-----ATTPTPARVPP 372
Db      305  ASTVFTVVLVNLHYRTPTETHDMGWTRNLLLYWIPWILMRKRGPHNLTYASLSTFKP 364
QY      373  PPDLERRSKSLANVLIDIDDDFRHPQAQPOQ-CRRYRGEENGAGLAA----- 423

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Db 365 -----NRHESLRINKDNEHSLSRANSFDACRLNQVIMQTSVNSGLTSLGSPSTM 417
Qy 424 HSCFGVDYELS-----LIL-----KEIRVITDQMRKDEADISRDWKFAAMVVDRLCLII 474
Db 418 ISSNGTTDVSOQATLILHRIYHELKIVTKRMIEGDKQEQACNNKFAAMVVDRLCLIV 477
Qy 475 FTLTFTIATLAVLSAPHIM 494
Db 478 FTTFIIVSTIGIFWSPAYLV 497
RESULT 8
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25671
R:Gattung, S.; Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25671
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-461 <GAT>
A:Cross-references: EMBL:U88167; PIDN: AAB42223.1; GSPDB:GN00019; CESP:D2092.3
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP:D2092.3
A:Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C:Superfamily: acetylcholine receptor

Query Match 42.8%; Score 1141; DB 2; Length 461;
Best Local Similarity 46.2%; Pred. No. 1.6e-91;
Matches 218; Conservative 85; Mismatches 121; Indels 48; Gaps 7;
Qy 34 EKRLHLLHDHYNVLRPVVNSDPLQLSFGTLFQIIVDDEKNOLLITNWKLEWMD 93
Db 26 ETKLEFDLLKGYNPLRPVNSQPLEVKIKFLQQLIDVDEKNQVSNAMLSYWFEDH 85
Qy 94 NLRWNTSDGGVVDLAVP--PHRLKPDVLMYNSADEGSDSTPTNVVNRNGSCLYVPP 151
Db 86 KIQWPKYGGIQQDIIRPGSSDHIMKPDVLLYNSAEDFDSTFKSNLLTYHTGVVWIPP 145
Qy 152 GIFKSTCKIDITWFPDDQRCMKFGSWTDVGOLDQLQDEGG-----DISFVTNGEW 207
Db 146 GVLKFCOLDVTFWFPDDQRCMKFGSWTFHGVAIDLQDDDTNGTQSMDLSTLYLVNGEW 205
Qy 208 ELIGVPGKNEIYNNCCPEYIDITFAVIRKTLTYFFNLIVPCVLIASMAILGFTLPP 267
Db 206 QVISTNAKRVSYKCCPEYPTVNYLHRRRTLYYGENLIIPSLISMAILGFMFPP 265
Qy 268 DSGEKLGLVITLLSLTVFLNVAETWTPATSDAVPLGLTYFCINMFVASSVSTLIIN 327
Db 266 DAGEKITLEVITLAIYVFLSVSEMTPTPTSEAVPLIGVFSCCMVWSASVYFTVVLN 325
Qy 328 YHHRHADTHEMSDWIRCVFLYVPLVLRMSRPGSATTPPARVPPPPDLELRSSKSL 387
Db 326 LHFRSADSHENPLVRVLLEFLPWLFPMSRPG-----YKFKV 363
Qy 388 ANYLIDDDFRHPQAOQPCCRYYRGEENGAGLAHSCFGVDYELSLIL-----KEIRV 442
Db 364 ANVIDSTDM-KPKKNPLDCNL-----PSNHAG-----YEAQILLHSHVHRELRR 408
Qy 443 ITDQMRKDEADISRDWKFAAMVVDRLCLIIFTLTFTIATLAVLSAPHIM 494
Db 409 VVAFYNKEEHDERIOTDWRFAAMVVDRLCLIIFTFTFIVISILAIMMSAPHII 460

RESULT 9
T19622
hypothetical protein C31H5.3 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T19622
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19622
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-560 <WIL>
A:Cross-references: EMBL:Z93778; PIDN: CAB07843.1; GSPDB:GN00019; CESP:C31H5.3
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.3
A:Map position: 1
A:Introns: 24/1; 70/3; 139/2; 270/1; 299/1; 336/3; 372/2; 456/3
C:Superfamily: acetylcholine receptor

Query Match 39.8%; Score 1060; DB 2; Length 560;
Best Local Similarity 37.6%; Pred. No. 2.5e-84;
Matches 217; Conservative 96; Mismatches 142; Indels 122; Gaps 11;
Qy 16 LLLLLCLLWPRGARC-----GYHEKRLHLLHDHYNVLRPVVNSDPLQLSFGTLQMQ 69
Db 9 VLSVSLIWE--TKSKVITWTDGHERLYAKLAENYKLRPVNRSEAAVVLGMDYQQ 66
Qy 70 IIDVDEKNOLLITNWKLEWMDNLRWNTSDFGVYKDLRVPHRLKPDVLMYNSADEG 129
Db 67 ILIDIDEKHQIMNSVWLRMSWTDHYLTWDPSEFGNKEVRLPINNWKPDVLYNSVDOQ 126
Qy 130 FDSYPTNVVNRNGSCLYVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGYQLDQ 189
Db 127 FDSWPNVNAVLYTGNVTWIPPAIRSSCAIDIAVFPEDTQHCMTKFGSWTYSGFTDL- 185
Qy 190 LQDEGGDISSFVT-----NGEWELIGVPGKNEIYNNCCPEYIDITFAVIRKTLTY 243
Db 186 -----INTTISPATYKPNGEWELLGTSQRSIFYECCPEYDYDTFTVSIRRTLY 237
Qy 244 YFNLIVPCVLIASMAILGFTLPPDSGEKLGLVITLLSLTVFLNVAETWTPATSDAVPL 303
Db 238 YGFLNLLPCMLISSLALLSFTLPADGEGKILNGVTIFMSLCVFMIMVAEMPOTSALPL 297
Qy 304 LGTYFCINMFVASSVSTLIINLYHHRHADTHE-MSDWIRCVFLYVPLVLRMSRPGSA 362
Db 298 IQIFYSCIMFQVGSVATVIALNFHRSPEQYKPNKFLKTLGLLGLWLTLLGMRPDV- 356
Qy 363 TTPPPARVPPDLEL-----RERSKSLANV-----L 391
Db 357 -----LELSVHGAYSDNKKKQOYLIEVERHILTRPNGNGHSAVDKAVHL 403
Qy 392 DIDDDFRHPQAOQPO-----CCRYRGGGEGA 419
Db 404 DLSTGNPHSDAKSSPKRTSASIMGMTGLPTQMGALDSSINKYCTKVTTRPLENGS 463
Qy 420 GLAAH-----SCFG-----VDYELSLILKEIRVITDQMRKDEADISR 458
Db 464 ATINHKSQPINNNNIYKCANNOQTQFDRHFHILNELRVISARVRKEAMHALQA 523
Qy 459 DNKFAAMVVDRLCLIIFTLTFTIATLAVLSAPHIMV 495
Db 524 DMFASRVYDVRCVFLAFAFLFMCTAIISYNAPHLEV 560

RESULT 10
T19862
hypothetical protein C40C9.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T19862
R:Hembry, C.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19188
A:Accession: T19862

A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-542 <WIL>
A:Cross-references: EMBL:D70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2
A:Experimental source: clone C40C9
C:Genetics:
A:Gene: CESP:C40C9.2
A:Map position: X
A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; 49
C:Superfamily: acetylcholine receptor

Query Match 39.6%; Score 1055.5; DB 2; Length 542;
Best Local Similarity 40.5%; Pred. No. 5.9e-84;
Matches 214; Conservative 94; Mismatches 136; Indels 85; Gaps 12;
QY 34 EKRLHLLHLDYVLPVNESDPLQLSFGTLTMOIIDVDEKKNOLLTNTWLKLENDM 93
DB 30 EYRLADLRHNDYPERVANASEPLVSVKIYLOQILDVDEKKNVITLVAMIEVQWTDY 89
QY 94 NLRWNTSFGGKDLRVP--PHRLWKPDVLMYNSADEGFDSTPTNVVVRNNGSCLYVPP 151
DB 90 KKWDPSEYGGKIDIRPCGNANA IWKPDVLLYNSADENFDSTPTPNVYVSYTGDVLIQVPP 149
QY 152 GIFKSTCKIDITWFPDQDORCEMKFGSWTYGYQLDLOLQ-----DEGGDISFVTN 204
DB 150 GILKLSCKIDITYFPDQDCHLKFGSWTYSNGFIDLRIINGPEGKNISDEGIDVQYVQN 209
QY 205 GEMELIGVPGKNEIYVNCPEPYDITFAVIRKTLTYFENLIVPCVLIASMALLGFT 264
DB 210 GEMNLAVPARHETNFD--EQYPSLFYLIQRTLYGLNLIFSLTSLMVLGFT 267
QY 265 LPDSEKLSGLVITLLSLTVFLNMVAETMPATSDAVPLL-----GTYNCFMFMVASS 318
DB 268 LPDAGEKITLITLLSVCFSLMVADMTPTSEAVPLIGLITFGAFFFSCCLMVVAS 327
QY 319 VYSTILILNYHRRHADTHMSDWIRCVFLYLPWVLRMSRG-----SATTPPPA 368
DB 328 VYFTVLNLNHRKPETHMSDFPRLLELLIWLPLLMLRRPEKTIFFNTHLKAKEEKA 387
QY 369 RV-----PPPPDLERSSKSLANV-----LDIDDDF--RH-----PQAQ 404
DB 388 KOGSKNGVGCKPDSVHPSEGLSLMKNIKLGRQOTIDFEYFHVQHNLMPVAPSEMT 447
QY 405 PQCC-----RYYRGEENGAGLAHSCFGVDYELSLILKEIRVITD 445
DB 448 PRVTSKYMAESYEDVYVMTLNQYQ-----KACL-----ELKNISSQTRAMRK 492
QY 446 QMRKDEADISRDWKFAAMVVDRLCLIFTIATLVLISAPHIM 494
DB 493 KHEEDERQAANDWKFAAMVVDRLCLITFSFIVVSTCGIMFSPHLI 541

RESULT 11
S12359
nicotinic acetylcholine receptor alpha-L1 chain precursor - desert locust
C:Species: Schistocerca gregaria (desert locust)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C:Accession: S12359
R:Marshall, J.; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.G.;
EMBO J. 9, 4391-4398, 1990
A>Title: Sequence and functional expression of a single alpha subunit of an insect nicot
A:Reference number: S12359; MUID:91092263; PMID:1702381
A:Accession: S12359
A:Molecule type: mRNA
A:Residues: 1-557 <MAR>
A:Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-557/Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <MAT
F:245-266/Domain: transmembrane #status predicted <TM1>
F:274-295/Domain: transmembrane #status predicted <TM2>
F:308-329/Domain: transmembrane #status predicted <TM3>

F:501-523/Domain: transmembrane #status predicted <TM4>
F:47,235/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 36.7%; Score 979; DB 2; Length 557;
Best Local Similarity 40.0%; Pred. No. 2.9e-77;
Matches 217; Conservative 88; Mismatches 160; Indels 78; Gaps 10;
QY 11 AAPAGLLLLCLLMPRGARCGYHEKRLLHLLHDYVLPVNVNEDPLQLSFGTLTMOI 70
DB 4 ALPMLLLLLLLLLLHHPAAAPDAKRLYDLDLLSNYNRLIRPVNNTDVLVKGRLSQL 63
QY 71 IDVDEKNOLLITNTWLKLENDMLRWNTSDFGGVKDLRVPVPHRLWKPDVLMYNSADGFG 130
DB 64 IDLALKDQILITNTWLEHEWQDHKFRWDPAEYGGVTELYVPSEHILWLDIVLYNNADGEY 123
QY 131 DSTYPTNVVVRNNGSCLVPPGIFKSTCKIDITWFPDQDORCEMKFGSWTYGYQLD-- 188
DB 124 VTTMTKAVLHHTGKVVWTPPAIFKSSCEIDVRFPPDQDQCFMKFGSWTYGQDIDLKH 183
QY 189 --QLQDEG---GGDISFVTNGEWELIGVPGKNEIYVNCPEPYDITFAVIRRRTL 242
DB 184 INQYDDNKVKVGDIDREYYPSEWMDILGVPAERHEKYYPCCAEYPDIFENITLRRKTL 243
QY 243 YFFNLIVPCVLIASMALLGFTLPDSEKLSGLVITLLSLTVFLNMVAETMPATSDAVP 302
DB 244 FYTNLIIVPCVIGISYLSVLVFLPADSGEKIALCISILLSQTMFFLLISEIIPSTSLAP 303
QY 303 LLGYFNCIMFMVASSVYSTILILNYHRRHADTHMSDWIRCVFLYLPWVLRMSRPGSA 362
DB 304 LLGXYLFTWVLVGLSVVITLVLNHYRKPSSTHKMAPWRKVRIRRLPKLLM----- 357
QY 363 TTPPPARVPPPDLELRSSKSLT-----ANVLDDDDFHRHQ 401
DB 358 -----RV---PEQLLADLASKRLLRHAAHNSLSAAAAAASAAASPDLSLRHHH 408
QY 402 AQQQCCRY-----YRGEENGAGLAH-----SFGVD----- 430
DB 409 LHQHQHQLHLHLQRPFGCGNLSATNREGGSAGAFGGPLSVVVGSLSDVATRKKY 468
QY 431 -YELSLILKEIRVITDQMRKODE--DADISRDWKFAAMVVDRLCLIFTIATLVL 488
DB 469 PFELEKAIHNVLFTQNHMQRODEDAE--DQDWGFVAMVLDRLFLWIFTIASIVGTFAILC 527
QY 489 SAP 491
DB 528 EAP 530
RESULT 12
A53956
nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human
C:Species: Homo sapiens (man)
C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
C:Accession: A53956; S21338
R:Milohovic, M.; Roses, A.D.
Exp. Neurol. 111, 175-180, 1991
A>Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuro
A:Reference number: A53956; MUID:91114756; PMID:1989896
A:Accession: A53956
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-503 <MIH>
A:Cross-references: GB:M37981; NID:g189252; PIDN:AAA59942.1; PID:g189253
R:Anand, R.; Lindstrom, J.
submitted to the EMBL Data Library, June 1990.
A:Description: Nucleotide sequence of the mature human nicotinic acetylcholine recept
A:Reference number: S21338
A:Accession: S21338
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 30-503 <ANA>
A:Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C:Genetics:

A:Gene: GDB:CHRNA3
A:Cross-references: GDB:125219; OMIM:118503
A:Map position: 15q24-15q24
C:Superfamily: acetylcholine receptor
C:Keywords: neurotransmitter receptor

Query Match 36.1%; Score 962; DB 2; Length 503;
Best Local Similarity 41.1%; Pred. No. 7.7e-76;
Matches 206; Conservative 89; Mismatches 172; Indels 34; Gaps 11;

QY 10 LAAPAG----LLLLLLPGRGARGYHEKRLHLLHLLHNNVLPVNVESDPLQLSGL 65
DB 6 LAAPGAVAPRLLLLSLLP-VARASEAHRLEFRLFEDYNEIIRPVANVSDDVIFHEF 64
QY 66 TLMQIIDVDEKQLITINLWLEWMDNLRNWTSDFGVKDLRVPVPHRLKPPDVLKYN 125
DB 65 SMSQLVKYDEVQIMETNMLKQIWNKYKLNWPSDYGGAEPVPAQKINPDIVLNN 124
QY 126 ADEGSDSYPTNVVNRNNGSCLYVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGY 185
DB 125 AVGFQVDDKTKALLKYTGVTWIPPAIFKSKCKIDVTYFPDYQNTMKFGSWYDRAK 184
QY 186 LDQLQDEGGDISFVTVNGEWELGVCKRNEIYVNCPEYIDITAVVIRKTLTYF 245
DB 185 IDLVIG-SSMNLKDYWESGEWAIIPKAGYKHDIKYNCCEIYDPDITSLYIRRLPFT 243
QY 246 FNLIYPCVLIASMALIGFTLPDSDGKLSLGTILLSLTVFLNMAETMPATSDAVPLIG 305
DB 244 INLIIPCLLSLTVLVLVPSDCGKVTCLISVLLSLTVLTVTEIPSTSLVPLIG 303
QY 306 TVFNCIMFVASSVSTILILNYHRRHADTHEMSDWIRCVFLYLPWVLRMSRP----GS 361
DB 304 EYLLETMTFVTLISIVTVFLNVHVRTPTHTMPSWVKTVFLNLLPRVFMFTRPTSNEG 363
QY 362 ATTPPARVPPPDLELRERS-SKSLANVLDDDDFRHQAQOQC-CRYYRGEEN- 417
DB 364 AOKPRLYGAELSNLCSFRAESKCKEG-----YP-CQDGMCGYCHRRITKSNF 413
QY 418 GAGLA-AHSCFGVDYELSL-----ILKEIRVITDOMRKDDDEDADISRDKFAAMV 467
DB 414 SANLRSSSESDAVLSLSALSPELKEAIOVKYIAENKKAQNEAKEIQDDWKYVAMV 473
QY 468 DRCLLIIFTFTIATLAVLL 488
DB 474 DRIFLWVFTVLCILGTAGLFL 494

RESULT 13
ACCH2N
nicotinic acetylcholine receptor alpha-2 chain precursor, neuronal - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C:Accession: S00377
R:Nef, P.; Oneyser, C.; Alliod, C.; Couturier, S.; Ballivet, M.
EMBO J. 7, 595-601, 1988
A:Title: Genes expressed in the brain define three distinct neuronal nicotinic acetylcholine receptors from Drosophila to
A:Reference number: S00376; MUID:88283624; PMID:3267226
A:Accession: S00377
A:Molecule type: DNA
A:Residues: 1-528 <NEF>
A:Cross-references: EMBL:X07339; NID:g62792; PIDN:CAB59645.1; PID:g6136914
C:Genetics:
A:Introns: 21/1; 73/3; 88/3; 125/2; 487/3
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-528/Product: nicotinic acetylcholine receptor predicted <SIG>
F:241-264/Domain: transmembrane #status predicted <TM1>
F:272-290/Domain: transmembrane #status predicted <TM2>
F:306-327/Domain: transmembrane #status predicted <TM3>
F:502-520/Domain: transmembrane #status predicted <TM4>
F:54,104/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:158-172,222-223/Disulfide bonds: #status predicted

Query Match 36.0%; Score 959; DB 1; Length 528;
Best Local Similarity 39.2%; Pred. No. 1.5e-75;
Matches 198; Conservative 84; Mismatches 161; Indels 62; Gaps 10;

QY 31 GYHEKRLHLLHLDHYNVLERPVNVSDPLQLSFGTLMQIIDVDEKQLITINILWLEW 90
DB 31 GFAEDRLFKHFTGYNRRSRPVPNTSDVIVAFGLSIAQLIDVDEKQMMTNNVWLKQW 90
QY 91 NDMNLRWNTSDGGVKDLRVPVPHRLKPPDVLKYNASDEGSDSYPTNVVNRNNGSCLYVP 150
DB 91 SDYKLRWNPEDDNTVSIRVPSEMIWIPDIVLYNNADGEFAVTHMKAHLFNSGKVKWP 150
QY 151 PGIFKSTCKIDITWFPDDQRCMKFGSWTYDGYQLDQLQDEGGDISFVTVNGEWELI 210
DB 151 PAIYKSSCSIDVTYFPDQONCKMKFGSWTYDKAKIDLE-NMEHHVLDLKYWESGEWAI 209
QY 211 GVPGRNRIYVNCPEYIDITFAVIRKTLTYFNFNLIVPCVLITASMALIGFTLPDSDG 270
DB 210 NAGRYNSKKYDCCTEYIPDITFYFVIRLRPLFTINLIIPCLLSLTVLTVLVPSCG 269
QY 271 EKLSLGVITLLSLTVFLNMAETMPATSDAVPLLGTYFNCIMFVASSVSTILILNYH 330
DB 270 EKITICISVLLSLTVFLLLITEIIPSTSLVPLIGEYLLFTWIFVTLSTIIIVFLNVH 329
QY 331 RHADTHEMSDWIRCVFLYLPWVLRMSRFSATTPPARVP-----PPDLELRERS 382
DB 330 RSPSTHTMPHWVRSFPLGFIPRWLFMKR-----PPLLPAEGTTGQYDPGTRL--ST 380
QY 383 SKSLANVLDDDDFRHQAQOQC-----CCRYRGEENGAGLAH-SC---- 426
DB 381 SCWLET--DVDDKWEIEEEEEEEEEEEKAYPSRVPSSGSG---GTOCHYSCEROA 435
QY 427 -----FGVDYELSL-----ILKEIRVITDOMRKDDDEDADISRDKFA 463
DB 436 GWASGGAPQVPLKGEVSGOGLTSLPSILRALSGVQYIADHLRAEDADFVKEDWKYV 495
QY 464 ANVVDRLCLIIIFTFTIATLAVLL 488
DB 496 ANVIDRFLWVFTIIVCLGTAGLFL 520

RESULT 14
ACFFAI
nicotinic acetylcholine receptor alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jun-2002
C:Accession: S00381; A38801
R:Bosny, B.; Ballivet, M.; Splierer, P.
EMBO J. 7, 611-618, 1988
A:Title: Conservation of neural nicotinic acetylcholine receptors from Drosophila to
A:Reference number: S00381; MUID:88283626; PMID:2840281
A:Accession: S00381
A:Molecule type: DNA
A:Residues: 1-567 <BOS>
A:Cross-references: GB:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A:Accession: A38801
A:Molecule type: mRNA
A:Residues: 1-567 <BO2>
A:Cross-references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576
A:Note: 538-Tyr was also found
C:Genetics:
A:Gene: FlyBase:nACR-alpha-96Aa
A:Cross-references: FlyBase:FBgn0000036
A:Map position: 3R 96A
A:Introns: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3
C:Superfamily: glycoprotein; ion channel; neurotransmitter receptor
C:Keywords: glycoprotein; signal sequence #status predicted <SIG>
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-567/Product: nicotinic acetylcholine receptor alpha-like chain #status predicted
F:224-240/Domain: extracellular #status predicted <EXT>
F:240-264/Domain: transmembrane #status predicted <TM1>
F:272-290/Domain: transmembrane #status predicted <TM2>

F:306-325/Domain: transmembrane #status predicted <TM3>
F:326-513/Domain: intracellular #status predicted <INT>
F:514-532/Domain: transmembrane #status predicted <TM4>
F:45,233/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:149-163,222-223/Disulfide bonds: #status predicted

Query Match 35.8%; Score 957.5; DB 1; Length 567;

Best Local Similarity 38.2%; Pred. No. 2.2e-75;

Matches 206; Conservative 86; Mismatches 174; Indels 73; Gaps 11;

QY 18 LLLCLLPARGARGCYHEKRLHLLHDHYNVLRPVVNESDPLQLSFGTLMOIDVDEKN 77

DB 9 VFIAHFATGGLANDPARLDYDLSNLRIRPVGNNSDRLLTVKMGRLSOLIDVNLKN 68

QY 78 QLLIINIKLEWDMNLRWNTSDFGGVKDLRVPVPHRLWKPDVLMYNSADEGFSYPTN 137

DB 69 QIMTTNVVEQEWNDYKLNKPPDDYGGVDTLHVPSEHIWHDPDVLVYNADGNVEYIMTK 128

QY 138 VVVRNGSCLVPPGIFKSTCKIDITWFFPDQRCMKFGSWYDGYQLDL----QLQD- 192

DB 129 AILHHTGKVVWKPPAIYKSFCEIDVEYFPFDEQTCFMKFGSWYDGYMVDLRHLKQTADS 188

QY 193 ---EGGDISFVTNGEWELICVPGKNEIYVNCPEYIDITFAVIRRKTLTYFFNLI 249

DB 189 DNIIEGIDLDQYIISVENDIMRPVAVRNEKIFYSCSEYLDIVFNLTRKTLFTYVNL 248

QY 250 VPCVLIASMALIGFTLPDPSGEKLSLGVITILLSLTVFLNMVAETMPATSDAVPLIGTYFN 309

DB 249 IPCVGISFLSVLFLVPLSDCEKISLISLSTVFLLELLAEIIPPTSLVPLLGKYL 308

QY 310 CIMFWASSVSTILILNYHHRHATHEMSDWIRCVFLYVLPWLVRMSRPGSATPPPAR 369

DB 309 FTMIVFVLSIYITVFLNVHYRTPTHTMPSWVKTVFLNLLPRVFMFTRPTSNEGNAQKP 366

QY 370 VPP-----PPDLE-LRERSKSL-----L 387

DB 367 QPPEVLTDVYHLPPDVFVNDYKRFSGDYGIPALPASHRFDLAAAGGISAHCFAPPL 426

QY 388 ANVLDI-----DDFRHPQAO----QPCCRYRYGGEENGAGLAHS-----CFGVDY--ELS 434

DB 427 PSSLPAGADDDLFSPSGLINGDISPGCC-----PAAAAAADAADLSPTKEKPYAREME 478

QY 435 LILKEIRVITDOMRKDEDEDADISRDKWFAAMVVDRLCLIIITLTIATLAVLSAPHI 493

DB 479 KTIEGSRFIAQHVKNKDKFESVEDWKYVAMVLDRLMFIACVWGTLIILOQPSL 537

RESULT 15

A37040

nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal (version 2) - human

C:Species: Homo sapiens (man)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 21-Jul-2000

C:Accession: A37040; S24595

R:Fornasari, D.; Chini, B.; Tarroni, P.; Clementi, F.

Neurosci. Lett. 111, 351-356, 1990

A:Title: Molecular cloning of human neuronal nicotinic receptor alpha-3-subunit.

A:Reference number: A37040; MUID:90245296; PMID:2336208

A:Accession: A37040

A:Molecule type: mRNA

A:Residues: 1-502 <FOR>

A:Cross-references: EMBL:X52239; NID:g177897; PIDN:AAC84176.1; PID:g177898

C:Superfamily: acetylcholine receptor

C:Keywords: neurotransmitter receptor; transmembrane protein

F:1-28/Domain: signal sequence #status predicted <SIG>

F:29-502/Product: nicotinic acetylcholine receptor alpha-3 chain #status predicted <MAT>

Query Match

Best Local Similarity 35.8%; Score 954; DB 2; Length 502;

Matches 203; Conservative 90; Mismatches 174; Indels 30; Gaps 10;

QY 10 LAAPAGLLLLCLLPARGCYHEKRLHLLHDHYNVLRPVVNESDPLQLSFGTLMOQ 69

DB 9 LACRARLLLLLSLLP-VARASEAERLFRLEFDYNEIIRPVANSDPVIHFEVMSQ 67

QY 70 IIDVDEKNQLLITNIWLKLEWDMNLRWNTSDFGGVKDLRVPVPHRLWKPDVLMYNSADEG 129

DB 68 LVKVDEVNQINMETNLWLKQIWNNDYKLNKPPSGYGAEMRPVPAQIKWPKDVLVYNNVAGD 127

QY 130 FDSHYPTNVVVRNNGSCLVPPGIFKSTCKIDITWFFPDQRCMKFGSWYDGYQLDLQ 189

DB 128 FOVTTKTKALLKYTGTEWTWIPPAIFKSSCKIDVTYFPFDYQNCNTMKFGSWSYDKAKIDLV 187

QY 190 LODEGGDISFVTNGEWELICVPGKNEIYVNCPEYIDITFAVIRRKTLTYFFNLI 249

DB 188 LIG-SSMNLKDYWSEGEWAIKAPGYKHDIKYNCCEEIYPDITYSLYRRPLPFTYINLI 246

QY 250 VPCVLIASMALIGFTLPDPSGEKLSLGVITILLSLTVFLNMVAETMPATSDAVPLIGTYFN 309

DB 247 IPCVLIISFLTVLFLVPLSDCEKVTICISLSTVFLVITETIPSTSLVPLIGEYLL 306

QY 310 CIMFWASSVSTILILNYHHRHATHEMSDWIRCVFLYVLPWLVRMSRPGSATPPPAR 365

DB 307 FTMIVFVLSIYITVFLNVHYRTPTHTMPSWVKTVFLNLLPRVFMFTRPTSNEGNAQKP 366

QY 366 PPARVPPPPDLELRERS-SKLLANVLIDDDFRHPQAOQPOC--CRYRGEEN-GAGL 421

DB 367 RPLYGAEISLNCFSRAESKCKEG-----YP-CQDGMCGYCHRRRIKISNFSANL 416

QY 422 A-AHSCFCGVYELSL-----ILKEIRVITDOMRKDEDEDADISRDKWFAAMVVDRLC 471

DB 417 TRSSSESVDADVLSLSALSPEIKAEIQSVKYIAENKQAQNEAKEIODDWKYVAMVIDRIF 476

QY 472 LIITLFTIATLAVLL 488

DB 477 LWVFTLVCILGTAGLFL 493

Search completed: August 13, 2003, 15:30:21

Job time : 20.5263 secs.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:30 ; Search time 43.5088 Seconds
(without alignments)
1809.483 Million cell updates/sec

Title: US-09-303-232-4

Perfect score: 2665

Sequence: 1 MCGRRARRSHLAAPAGLLILL.....LFTTIATLAVLLSAPHIMVS 496

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2665	100.0	496	21	AA198015
2	1850	69.4	770	21	AA198014
3	1803.5	67.7	501	21	AA198016
4	1417.5	53.2	311	22	ABB63683
5	1267	47.5	502	18	AA123368
6	1253	47.0	498	22	ABB60432
7	1246	46.8	502	15	AAW44153
8	1246	46.8	502	21	AAW09025
9	1246	46.8	502	21	AAW24088

10	1246	46.8	502	22	AAW82690	Nicotinic acetylch
11	1246	46.8	502	22	AAW50012	Wild-type human al
12	1246	46.8	502	23	ABB82435	Human neuronal NAC
13	1246	46.8	502	23	ABG70492	Human neuronal nic
14	1242	46.6	502	19	AAW69216	V274T variant huma
15	1240	46.5	502	22	AAW50015	Mutant human alpha
16	1236	46.4	502	22	AAW50016	Mutant human alpha
17	1230	46.4	502	22	AAW50017	Mutant human alpha
18	1219.5	45.8	511	18	AAW12369	Neuronal alpha-bun
19	1053.5	39.5	554	22	AAE12824	Caenorhabditis ele
20	1053.5	39.5	554	24	ABP96318	Caenorhabditis ele
21	989	37.1	470	22	AAW50014	Chimeric alpha7/5-
22	984	36.9	448	22	AAW50018	Mature cell surfac
23	965	36.2	193	22	ABB60716	Drosophila melanog
24	964.5	36.2	631	23	AAO17243	Modified acetylcho
25	960	36.0	504	18	AAW09022	Neuronal nicotinic
26	960	36.0	529	15	AAW44155	Human neuronal nic
27	960	36.0	529	16	AAW73966	Alpha 2 subunit of
28	960	36.0	529	18	AAW09021	Neuronal nicotinic
29	960	36.0	529	23	ABB82430	Human neuronal NAC
30	960	36.0	529	23	ABG31800	Human neuronal nic
31	960	36.0	529	23	ABG61850	Prostate cancer-as
32	954	35.8	622	23	AAO17245	Modified acetylcho
33	954	35.8	622	23	ABB08885	Modified acetylcho
34	926	34.7	576	22	ABB61954	Modified hen ACR s
35	918	34.4	494	18	AAW09018	Drosophila melanog
36	918	34.4	494	18	AAW09018	Neuronal nicotinic
37	918	34.4	494	23	ABG70491	Human neuronal NAC
38	914	34.3	580	22	ABG62727	Human neuronal nic
39	910	34.1	504	15	AAW44156	Human neuronal NAC
40	910	34.1	504	23	ABB82431	Human neuronal NAC
41	910	34.1	504	23	ABG70488	Human neuronal nic
42	906.5	34.0	502	23	AAE15160	Human mutant neuro
43	906.5	34.0	631	23	AAO17244	Modified acetylcho
44	906.5	34.0	631	23	ABB08884	Modified hen ACR s
45	903.5	33.9	498	18	AAW09027	Neuronal nicotinic

ALIGNMENTS

RESULT 1

AA198015
ID AA198015 standard; Protein; 496 AA.

XX AC

XX AC

XX AC

XX AC

DT 17-FEB-2000 (first entry)

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

XX AC

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XX AC

XX AC

QY 2 GGRARRSHLAAPAGLILLCLLWPRGARGCYHEKRLHLLDHYNVLPRPVNESDPLQ 61
DB 16 GGRM-----LVYGLGLIMI-----PACAGPHEKRLHLLDHYNVLPRPVNESDPLQ 66
QY 62 SFGTLMLQIIDVDEKNOLLITNIWLKLEWMDNMLRWNTSDFGGVKDLRVPVPHRLWKPDVL 121
DB 67 SFGTLMLQIIDVDEKNOLLITNIWLKLEWMDNMLRWNTSDFGGVKDLRVPVPHRLWKPDVL 126
QY 122 MNSADEGFDSTYPTNVVNRNGSCLYVPPGIFKSTCKIDITWFPDDQRCMEKFGSWTY 181
DB 127 MNSADEGFDSTYPTNVVNRNGSCLYVPPGIFKSTCKIDITWFPDDQRCMEKFGSWTY 186
QY 182 DGYQLDLQDEGGDISFVTNGEWELIGVPGKRNEIYYNCCPEYIDITFAVIRRK 241
DB 187 DGYQLDLQDEGGDISFVTNGEWELIGVPGKRNEIYYNCCPEYIDITFAVIRRK 246
QY 242 LYFFNLIVPCVLTIASALLGFTLPPDSGKLSLGVTLISLTVFLNVAETMPATSDAV 301
DB 247 LYFFNLIVPCVLTIASALLGFTLPPDSGKLSLGVTLISLTVFLNVAETMPATSDAV 306
QY 302 PLLG 305
DB 307 PLLG 310

RESULT 5
AAW12368
ID AAW12368 standard; Protein; 502 AA.
XX AC AAW12368;
XX DT 17-JUN-1997 (first entry)
XX DE Neuronal alpha-bungarotoxin binding protein alpha subunit.
XX KW Neuronal alpha-bungarotoxin binding protein alpha 1; cholinergic;
XX LW ligand binding; ion channel.
XX OS Gallus sp.
XX FH Key Location/Qualifiers
XX FT Peptide 1..22
XX FT Protein /label= Sig_peptide
XX FT 23..502 /label= Mat_protein
XX US5599709-A.
XX PD 04-FEB-1997.
XX PF 28-SEP-1989; 89US-0413947.
XX PR 28-SEP-1989; 89US-0413947.
XX PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX PI Lindstrom JM, Schoepfer RD;
XX DR WPI; 1997-118297/11.
XX DR N-PSDB; AAT59196.

New isolated neuronal alpha-bungarotoxin-binding protein DNA - used to screen cholinergic agents and other drugs which may affect ligand binding, ion channel or other activities of the protein.
XX Example; Fig 2A-B; 18pp; English.
XX The alpha1 subunit (AAW12368) and alpha2 subunit (AAW12369) amino acid sequences of chick neuronal alpha-bungarotoxin binding protein (ABBP) were deduced from newly isolated DNA molecules (AAT59196-97) CC obtd. from an 18-day chick embryo cDNA library. ABBP subunits can CC be produced in recombinant host cells, pref. a bacterium, and used

CC in the screening of cholinergic agents and other drugs that may affect the ligand binding, ion channel or other activity of intact CC ABBP subtypes. The ABBP alpha1 and alpha2 subunits can also be CC used to produce subunit peptides for use as immunogens for CC preparing antibodies to permit affinity purification of subtypes CC and their histological location.

XX SQ Sequence 502 AA;
Query Match 47.5%; Score 1267; DB 18; Length 502;
Best Local Similarity 48.6%; Pred. No. 5.6e-118;
Matches 249; Conservative 83; Mismatches 144; Indels 36; Gaps 6;
QY 1 MGRARRSHLAAPAGLILLCLLWPRGARGCYHEKRLHLLDHYNVLPRPVNESDPLQ 60
DB 1 MGLRALMLWLLAAAGLV-----RESLQGEFORKLYKELLYNPLRPFVANDSPLT 52
QY 61 LSFGTLMLQIIDVDEKNOLLITNIWLKLEWMDNMLRWNTSDFGGVKDLRVPVPHRLWKPDV 120
DB 53 VYFTLSLMLQIIDVDEKNOLLITNIWLKLEWMDNMLRWNTSDFGGVKDLRVPVPHRLWKPDV 112
QY 121 LMNSADEGFDSTYPTNVVNRNGSCLYVPPGIFKSTCKIDITWFPDDQRCMEKFGSWT 180
DB 113 LLYNSADERFDTFTNTVLVNSGHCQYLPFGIFKSSCYIDVRWFPDQVCKNLKFGSWT 172
QY 181 YDGYQLDLQDEGGDISFVTNGEWELIGVPGKRNEIYYNCCPEYIDITFAVIRRK 240
DB 173 YGGWSLDLQOE---ADISGYISNGEWDLVGPGRKTESFYECCKEPEYDITFTVTRRR 229
QY 241 TLYFFNLIVPCVLTIASALLGFTLPPDSGKLSLGVTLISLTVFLNVAETMPATSDA 300
DB 230 TLYTGLNLLIPCVLTIASALLGFTLPPDSGKLSLGVTLISLTVFLNVAETMPATSDS 289
QY 301 VPLLGTYNFNCIMFVAVSVVSTILILNHHADTHHEMSDWIRCVFLYVLPVLRMSRPG 360
DB 290 VPLIAQYFASTMIIVGLSVTVIVLYVHHDPDGGKMPKTRVILLNWCWAFELRMKRP 349
QY 361 SATPPPARVPPPPDLELRSSKSLANVLD-----IDDDFRHPQAOQ 404
DB 350 E-----DKVRPACQHKQRCCLSSMEMNTVSGQCSNGNMLYIGFRGLDGVHCTPTTDS 403
QY 405 PQCCRYVRGG--EENGAGLAHSCFVDYELSLILKEIRVITDQMRKDEADISRDWKF 462
DB 404 GVICGRWTCSPTEENLLHSGHPSEG-DPDLAKILEEVRYIANFRDQDEEAICNEWKF 462
QY 463 AAMVVDRLCLIIFTIATLAVLLSAPHIM 494
DB 463 AASVVDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 6
ABB60432
ID ABB60432 standard; Protein; 498 AA.
XX AC ABB60432;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 8088.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.

II. RESULT

Db 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKWTRVILLNWCANFLRMKRPGEDKVRPACQHK 36

```

QY 361 -----SATTTPPPAR-----VPPPPDLELRSSKSLANVLD 392
Db 361 QRRCSLASVEMSAVAPPASGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPH- 416
QY 393 IDDDFRHPOAQOCCRYRGGENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDE 452
Db 417 -DEHLLH-----GGQPPEG-----DPLAKILEEVRIANRRCODE 452
QY 453 DADISRDWKFAMVVDRLCLIIFTLTIIATLAVLSAPHIM 494
Db 453 SEAVCSEWKFACVVDRLCLMAFSVFTIICIGILMSAPNFV 494

RESULT 12
ID ABB82435
XX ABB82435 standard; Protein; 502 AA.
AC ABB82435;
XX
DT 22-JAN-2003 (first entry)
DE Human neuronal NACHr alpha7 subunit.
XX
KW Human; neuronal; nicotinic acetylcholine receptor; NACHr; drug screening;
KW Immunohistochemistry; NACHr alpha7 subunit; receptor.
XX
OS Homo sapiens.
XX
PN WO200259266-A2.
XX
PD 01-AUG-2002.
XX
PF 29-OCT-2001; 2001WO-US50985.
PR 01-NOV-2000; 2000US-0703951.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Gillespie A, Claeps BO, Chavez-Noriega LE, Siegel R, Elliott KJ;
DR WPI; 2002-698532/75.
DR N-PSDB; ABV73248.
XX
XX Cell comprising nucleic acids encoding human alpha and beta subunits of
PT neuronal nicotinic acetylcholine receptors, useful for in vitro
PT screening of a drug substance in a test system specific for humans
XX
PS Examples; Page 130-131; 143pp; English.
XX
CC The invention relates to a suitable host cell transfected with an
CC isolated nucleic acid molecule comprising a sequence of nucleotides or
CC ribonucleotides that encodes at least one alpha or beta subunit of a
CC human neuronal nicotinic acetylcholine receptor (NACHr). The compositions
CC and methods of the present invention, which provide a means to prepare
CC synthetic or recombinant receptors and receptor subunits that are
CC substantially free of contamination from many other receptor proteins,
CC are useful for observing the effect of a drug substance on a particular
CC subtype to perform in vitro screening of the drug substance in a test
CC system that is specific for humans. The antibodies can be used in
CC immunochemistry and for diagnostic and therapeutic applications. The
CC present sequence represents a human neuronal NACHr alpha7 subunit.
XX
SQ Sequence 502 AA;
Query Match 46.8%; Score 1246; DB 23; Length 502;
Best Local Similarity 46.0%; Pred. No. 7.2e-116;
Matches 240; Conservative 86; Mismatches 126; Indels 70; Gaps 6;
QY 12 APAGLLLLCLLPRGARGGYHEKRLHLLHLDHYNVLERPVVNESDPLQLSFGLTMOII 71
Db 4 SPGGWLAALASLLHVSLOGEFQRKLYELVKNYNPLRPVANDSQPLTVYFSLQLIM 63

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QY 72 DVDEKNQLITNWLKLEWDMNLRNTSDFGGVKDLRVPPHRLMKPDVLMYNSADEGPD 131
Db 64 DVDEKNQLITNWLKLEWDMNLRNTSDFGGVKDLRVPPHRLMKPDVLMYNSADEGPD 123
QY 132 STYPTNVVNRNNGSCLYPPGIFKSTCKIDITWFFPDDOORCEMKSGSWTYDGYOLDLQLO 191
Db 124 ATFTNVLNVNNGHCOYLPPIGIFKSTCKIDITWFFPDDOORCEMKSGSWTYDGYOLDLQLO 183
QY 192 DEGGDGISSFTNGEWELIGVPGKNEIYNGCCPEYIDITFAVIRRRKTLTYFFNLIVP 251
Db 184 E---ADISGYIPNGENDLVGIFGKSEREYECCKEYPDVTFTVTRRTLYYGLNLLIP 240
QY 252 CVLIASMLLFTLPDPSGKLSLGVITLLSTVFLNMVAETMPATSDAVPLLGYFNCI 311
Db 241 CVLISALALLVFLPADSGEKISLGITVLLSTVFLNMVAETMPATSDAVPLIAGVFAST 300
QY 312 MEMVASSVSTILILNYHHRHADTHEMSDWIRCVLYLWLPWLKRSRPG----- 360
Db 301 MIIVGLSVVTVIVIOYHHDDPDGGMKPMKTRVILLNMCAMFLMRKRPGEKVRPACQHK 360
QY 361 -----SATTTPPPAR-----VPPPPDLELRSSKSLANVLD 392
Db 361 QRRCSLASVEMSAVAPPASGNLLYIGRGLDGVHCVPTPDSGVVCGRMACSPH- 416
QY 393 IDDDFRHPOAQOCCRYRGGENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDE 452
Db 417 -DEHLLH-----GGQPPEG-----DPLAKILEEVRIANRRCODE 452
QY 453 DADISRDWKFAMVVDRLCLIIFTLTIIATLAVLSAPHIM 494
Db 453 SEAVCSEWKFACVVDRLCLMAFSVFTIICIGILMSAPNFV 494

RESULT 13
ABG70492
ID ABG70492 standard; Protein; 502 AA.
XX
AC ABG70492;
XX
DT 06-DEC-2002 (first entry)
DE Human neuronal nicotinic acetylcholine receptor alpha 7 subunit.
XX
KW Human; neuronal nicotinic acetylcholine receptor; nNACHr; receptor;
KW ion flux; alpha 7 subunit.
XX
OS Homo sapiens.
XX
PN US6440681-B1.
XX
PD 27-AUG-2002.
XX
PF 07-JUN-1995; 95US-0487596.
XX
PR 03-APR-1990; 90US-0504455.
PR 30-NOV-1992; 92US-0938154.
PR 08-MAR-1993; 93US-0028031.
PR 08-NOV-1993; 93US-0149503.
XX
PA (MERI ) MERCK & CO INC.
XX
PI Elliott KJ, Ellis SB, Harpold MM;
XX
DR WPI; 2002-711528/77.
DR N-PSDB; ABS54875.
XX
XX Identifying antagonists or agonists of human neuronal nicotinic
PT acetylcholine receptors, by contacting recombinant cells with test
PT compound, and measuring ion flux of cells or binding of compound to
PT nNACHr
XX
PS Claim 101; Column 59-64; 56pp; English.
XX

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CC The invention relates to a method for identifying compounds that are
 CC antagonists or agonists of human neuronal nicotinic acetylcholine
 CC receptors (nAChRs), by contacting recombinant cells with a test
 CC compound and measuring ion flux, the electrophysiological response of the
 CC cells or binding of the test compound to the nAChR. The recombinant
 CC cells are produced by transfection with a nucleic acid encoding at least
 CC one human nAChR (alpha or beta) subunit, such that the cells express an
 CC nAChR comprising one human subunit encoded by the transfected nucleic
 CC acid. This sequence represents the alpha 7 subunit of the human nAChR
 CC polypeptide.

XX SQ Sequence 502 AA;

Query Match 46.8%; Score 1246; DB 23; Length 502;
 Best Local Similarity 46.0%; Pred. No. 7.2e-116;
 Matches 240; Conservative 86; Mismatches 126; Indels 70; Gaps 6;

Qy 12 APAGLLLLCLLWPRGARGCYHEKRLHLLHDHYNVLERPVVNESDPLQSLFGLTLMQII 71
 Db 4 SPGGVWLAALASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIM 63

Qy 72 DVDEKNOLLITNIWKLWMDMLNRWNTSDFGVKDLRVPVPHRLWKPDLVLMYNSADEGFD 131
 Db 64 DVDEKNQVLTNTIWLQSWTDHYLQWNVSEYPGVKTVPFDDGQIWKPDILLYNSADERFD 123

Qy 132 STYPTNVVNRNGLVPPGIFKSTCKIDITWPFDDQRCMKFGSWTYDGYLDLQIQ 191
 Db 124 ATHTNVLNVSSGHCQYLPPIKFSYIDVRWPFDDVQHCCLKFGSWSGYSLDLQMQ 183

Qy 192 DEGGDISFVTNGEWELIGVPGKRNIEIYNCCEPYDITFAVIRKTKLYFFNLIIVP 251
 Db 184 E---ADISGYPNGEWDLVIGPKRSERFECCKEYPDVTFTVMRRRTLYGLNLLIP 240

Qy 252 CVLIASALLGFTLPDPSGKLSLGVITLLSLTVFLNVAETPATSDAVPLLTGYFNCI 311
 Db 241 CVLISALLVFLPADSGEKISLGVITLLSLTVFLNVAETPATSDSVPLIAQYFAS 300

Qy 312 MFVAVSSVSTILINLHHHADTHEMSDWIRCVLYLWLPVLMYNSADEGFD 360
 Db 301 MIIVGLSVVTVIVLYVHHDDPDGKMPKWTIRVILLNWCAMFLRMKRPGEKVRPACQHK 360

Qy 361 -----SATTPPPAR-----VPPPPDLELRSSKSLANVLD 392
 Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLGDVHCVPVPDSCVGVCGMACSPH 416

Qy 393 IDDFRHPQAQPOCCRYRGEENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDE 452
 Db 417 -DEHLH-----GGQPEG-----DPLAKTLEEVRYIANFRQDE 452

Qy 453 DADISRWKFAAMVVDRLCLIFTLTIATLAVLLSAPHIM 494
 Db 453 SEAVCSEWKAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494

RESULT 14

AAW69216
 ID AAW69216 standard; Protein; 502 AA.

XX AC AAW69216;

XX DT 09-OCT-1998 (first entry)

XX DE V274T variant human alpha7 nAChR protein.

XX KW Alpha7 nAChR; alpha7 nicotinic acetylcholine receptor subunit; cancer;
 KW neurodegeneration; enzyme dysfunction; affective disorder; therapy;
 KW immune dysfunction; diabetic neuropathy; Alzheimer's disease;
 KW schizophrenia.

XX OS Homo sapiens.

XX PN W09828331-A2.

XX

PD 02-JUL-1998.

XX 22-DEC-1997; 97MO-US23405.

XX 20-DEC-1996; 96US-0771737.

XX (ABBO) ABBOTT LAB.

XX Briggs CA, Gopalakrishnan M, McKenna DG, Monteggia LM;
 PI Roch J, Sullivan JP, Touma E;

XX WPI; 1998-377593/32.

DR N-PSDB; AAV44687.

XX Nucleic acid encoding variant of human alpha7 nicotinic
 PT acetylcholine receptor sub-unit - used to identify modulators of
 PT the receptor, potentially useful for treating neuro-degeneration,
 PT cancer, affective disorders etc.

XX Claim 15; Fig 2; 4app; English.

XX This sequence is the V247T variant of human alpha7 nicotinic
 CC acetylcholine receptor (nAChR) subunit of the invention. Cells containing
 CC the DNA are used to express the protein and to identify modulators of
 CC alpha7 nAChR activity or cytoprotective agents, e.g. antisense
 CC compounds or antagonists that are potentially useful for treating
 CC neurodegeneration, enzyme dysfunction, affective disorders and immune
 CC dysfunction, such as cancer, post-herpetic neuralgia, diabetic
 CC neuropathy, osteoarthritis, Alzheimer's or Parkinson's diseases, kuru,
 CC psychosis and schizophrenia. Probes based on the DNA are used to detect
 CC the DNA in usual hybridization or amplification tests, while monoclonal
 CC antibodies are used to detect the protein for diagnosis (in vitro or by
 CC in situ immuno-fluorescent assay). Compared with wild-type alpha7 nAChR,
 CC the protein has about 100-fold greater sensitivity to cholinergic
 CC receptor agonists (nicotine or acetylcholine) and response to these
 CC agonists decays more slowly, but the wild-type inward rectification is
 CC retained.

XX SQ Sequence 502 AA;

Query Match 46.6%; Score 1242; DB 19; Length 502;
 Best Local Similarity 45.8%; Pred. No. 1.8e-115;
 Matches 239; Conservative 86; Mismatches 127; Indels 70; Gaps 6;

Qy 12 APAGLLLLCLLWPRGARGCYHEKRLHLLHDHYNVLERPVVNESDPLQSLFGLTLMQII 71
 Db 4 SPGGVWLAALASLLHVSLOGEFORKLYKELVKNYNPLERPVANDSQPLTVYFSLSLQIM 63

Qy 72 DVDEKNOLLITNIWKLWMDMLNRWNTSDFGVKDLRVPVPHRLWKPDLVLMYNSADEGFD 131
 Db 64 DVDEKNQVLTNTIWLQSWTDHYLQWNVSEYPGVKTVPFDDGQIWKPDILLYNSADERFD 123

Qy 132 STYPTNVVNRNGLVPPGIFKSTCKIDITWPFDDQRCMKFGSWTYDGYLDLQIQ 191
 Db 124 ATHTNVLNVSSGHCQYLPPIKFSYIDVRWPFDDVQHCCLKFGSWSGYSLDLQMQ 183

Qy 192 DEGGDISFVTNGEWELIGVPGKRNIEIYNCCEPYDITFAVIRKTKLYFFNLIIVP 251
 Db 184 E---ADISGYPNGEWDLVIGPKRSERFECCKEYPDVTFTVMRRRTLYGLNLLIP 240

Qy 252 CVLIASALLGFTLPDPSGKLSLGVITLLSLTVFLNVAETPATSDAVPLLTGYFNCI 311
 Db 241 CVLISALLVFLPADSGEKISLGVITLLSLTVFLNVAETPATSDSVPLIAQYFAS 300

Qy 312 MFVAVSSVSTILINLHHHADTHEMSDWIRCVLYLWLPVLMYNSADEGFD 360
 Db 301 MIIVGLSVVTVIVLYVHHDDPDGKMPKWTIRVILLNWCAMFLRMKRPGEKVRPACQHK 360

Qy 361 -----SATTPPPAR-----VPPPPDLELRSSKSLANVLD 392
 Db 361 QRCCLASVEMSAVAPPASNGNLLYIGFRLGDVHCVPVPDSCVGVCGMACSPH 416

Qy 393 IDDFRHPQAQPOCCRYRGEENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDE 452

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Db 417 -DEHLLH-----GGOPPEG-----DPLAKILEEVRYIANRFRQDE 452
QY 453 DADISRDWKFAAMVVDRLCLIIFTLTIIATLAVLSAPHIM 494
Db 453 SEAVCSWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494

RESULT 15
AAB50015
ID AAB50015 standard; Protein; 502 AA.
XX
AC AAB50015;
XX
DT 14-MAR-2001 (first entry)
XX
DE Mutant human alpha7 ligand gated ion channel #1.
XX
KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
5-hydroxytryptamine; 5-HT3; calcium ion conductance; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 230 /note= "Wild-type Thr substituted by Pro"
FT
PN W0200073431-A2.
XX
PD 07-DEC-2000.
XX
PF 25-MAY-2000; 2000WO-US11862.
XX
PR 27-MAY-1999; 99US-0136174.
XX
PA (PHAA ) PHARMACIA & UPJOHN CO.
XX
PI Groppi VE, Wolfe ML, Berkenpas MB;
XX
DR WPI; 2001-061524/07.
DR N-PSDB; AAC90385.
XX
PT Special cell culture medium for treating cells and for inducing
mammalian cell lines to conduct calcium ions, comprising specified
concentrations of ions of sodium, calcium and potassium at specified pH
XX
PS Claim 100; Pages 70-72; 77pp; English.
XX
CC The present sequence is a mutant human alpha7 nicotinic acetylcholine
gated ion channel. The human alpha7 ion channel was used in the
construction of an alpha7/5-hydroxytryptamine (5-HT3) chimeric ligand
gated ion channel (see AAC90382 and AAB50014). The alpha7/5-HT3 chimeric
ion channel can be expressed by recombinant cells in the present
invention, resulting in preferential calcium ion conductance by the
cells.
XX
SQ Sequence 502 AA;

Query Match 46.5%; Score 1240; DB 22; Length 502;
Best Local Similarity 45.8%; Pred. No. 2.9e-115;
Matches 239; Conservative 86; Mismatches 127; Indels 70; Gaps 6;

QY 12 APAGLLLLLCLLPARGCYHEKRLHLHDHYNVLRPVVNESDPLQLSFGLTLMQII 71
Db 4 SPCGVWLAAASLLHVSLOGEFQKLYKELVKNPLRPVANDSQPLTVFSLSLQIM 63
QY 72 DVDEKNQLITNLWLKNWMDNLRWNTSDFGVKDLRVPPHRLMKPDMVLMYNSADEGFD 131
Db 64 DVDEKNQVLTNLWLQMSWDHVLQWNVSEYFGVKTVPFDGQWKPDILLYNSADERFD 123
QY 132 STYPTNVVVRNNGSCLYVPPGIFKSTCKIDITWFFPDORCEMKFGSWTYDGYQLDLQ 191
```

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Db 124 ATFTTNVLNSSGHCQYLPPIGFKSCYIDVRNPFDFVQHCKLKFGWSYSGWSLQMQ 183
QY 192 DEGGDISSFVTNGEWELIGVPGKRNEIYNNCCPEPYDITFAVWIRRKLTLYFFENLIVP 251
Db 184 E---ADISGYIPNGEWDLVGIPGKRSERFYECCKEPDPDFTVTWRRRPLYTGLNLLIP 240
QY 252 CVLIASMALGFTLPPDSGEKLSLGVITILSLTVFLNMVAETMPATSDAYPLLGTYFNCI 311
Db 241 CVLISALALLVFLLPADSGEKISLIGITVLLSLTVFLLVAEIMPATSDSVPLIAQYFAST 300
QY 312 MFWVASSVSTILILNYHRRHADTHEMSDWIRVCVFLYWLWPLRMSRPG----- 360
Db 301 MIIVGLSVVTVIVLQYHHHDPDGGKMPKWTIRVILLNWCWAFLRMKRPGEDKYRPACQHK 360
QY 361 -----SATTTPPAR-----VPPPPDLELRERSKSLIANVLD 392
Db 361 QRCRSIASVEMSAVAPPASNGNLLYIGFGLDGVHCVPDPTDSGVVCGRMACSPTH---- 416
QY 393 IDDDFRHPQAQQPCCCRYRGRGEENGAGLAHSCFGVDYELSLILKEIRVITDQMRKDD 452
Db 417 -DEHLLH-----GGOPPEG-----DPLAKILEEVRYIANRFRQDE 452
QY 453 DADISRDWKFAAMVVDRLCLIIFTLTIIATLAVLSAPHIM 494
Db 453 SEAVCSWKFAACVVDRLCLMAFSVFTIICTIGILMSAPNFV 494
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Search completed: August 13, 2003, 15:25:26
Job time : 44.5088 secs

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OM nucleic - nucleic search, using sw model

Run on: August 21, 2003, 03:48:31 ; Search time 3249.96 Seconds
(without alignments)
11127.831 Million cell updates/sec

Title: US-09-303-232-3_COPY_335_1822

Perfect score: 1488

Sequence: 1 atggcgggcgggcgccg.....cgccacacatcatgtgtcg 1488

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*
2: em_esthum.*
3: em_estlin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_htc.*
9: gb_estl.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pin.*
20: em_gss_vit.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gssi.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	476.2	32.0	885	10	BG632919
2	320.6	21.5	1201	9	AL530299
3	281.6	18.9	1864	11	AK053497
4	281.6	18.9	2916	11	AK051730

5	281.6	18.9	3126	11	AK080415	Mus muscu
6	280.4	18.8	4290	11	AK029177	Mus muscu
7	269.4	18.1	607	9	AI292581	GH15518.5
8	263.4	17.7	2010	11	AK080475	Mus muscu
9	258	17.3	4037	11	AK049722	Mus muscu
10	258	17.3	4046	11	AK051742	Mus muscu
11	253.8	17.1	2940	11	AK034228	Mus muscu
12	253.8	17.1	3230	11	AK083157	Mus muscu
13	245.2	16.5	908	13	BU149265	AGENCOURT
14	244.4	16.4	3483	11	AK081254	Mus muscu
15	241.4	16.2	615	14	CB149460	K-EST0205
16	236.8	15.9	1034	13	EX403124	EX403124
17	232.8	15.6	922	13	BU915857	AGENCOURT
18	226.2	15.1	410	12	BI516733	BI516733
19	225.2	15.1	410	12	BI516843	BI516843
20	214.6	14.4	833	14	CB245337	UT-M-FY0-
21	213.8	14.4	640	14	CB244439	UT-M-FY0-
22	213.8	14.4	1101	29	CNS0001F	AL038211
23	212.8	14.3	1007	29	CNS000HJU	AL073676
24	208	14.0	1036	13	EX437801	EX437801
25	203.8	13.7	978	29	CNS006F9	AL064281
26	202	13.6	720	14	CA373069	CA373069
27	199.6	13.4	2513	11	AK033068	Mus muscu
28	198	13.3	755	10	AW914206	AW914206
29	191.6	12.9	864	9	AU120692	AU120692
30	189.6	12.7	658	12	BM711715	BM711715
31	187.4	12.6	755	13	BU702422	BU702422
32	187.2	12.6	818	13	BU161024	BU161024
33	184.4	12.4	1201	13	EX421718	EX421718
34	183.4	12.3	2074	11	AK087554	AK087554
35	182.2	12.2	939	13	BQ720344	BQ720344
36	181.8	12.2	763	14	CA374163	CA374163
37	178.2	12.0	586	13	EX299163	EX299163
38	177.8	11.9	3827	11	AK041217	Mus muscu
39	175.8	11.8	797	14	CA326954	CA326954
40	172.6	11.6	882	12	BI195149	BI195149
41	172	11.6	754	29	CNS02R2B	AL210044
42	168.8	11.3	4589	11	AK030464	Mus muscu
43	168	11.3	1835	11	AK010496	Mus muscu
44	167.2	11.2	554	10	BE664308	BE664308
45	166	11.2	932	29	CNS02DCP	AL192274

ALIGNMENTS

RESULT 1

BG632919/c

LOCUS

DEFINITION

BG632919 885 bp mRNA linear EST 23-APR-2001
GH16126.3prime GH Drosophila melanogaster head pot2 Drosophila
melanogaster cDNA clone GH16126.3 similar to CG4128; Fban0004128
'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd

Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Based upon the presence of a XhoI site followed by a run of 14 or

more T residues at the beginning of the sequence, this clone was polyadenylated. The resulting poly-T sequence has been removed. hit genomic AB003511: arm: X [18792641,19136447] estimated-cyto:18A3-18C6: 04/10/2001 Plate: GH.161 row: C column: 2 High quality sequence stop: 784.

FEATURES

source

Location/Qualifiers

1..885

/organism="Drosophila melanogaster"

/mol_type="mRNA"

/db_xref="taxon:7227"

/clone="GH16126"

/sex="male and female"

/dev_stage="adult"

/lab_host="DH5 - alpha"

/clone_lib="GH Drosophila melanogaster head pot2"

/note="Organ: head; Vector: pot2; Site_1: EcorI; Site_2:

XhoI; Sized fractionated cDNAs were directly ligated into

pot2. Plasmid cDNA library."

pot2. Plasmid cDNA library."

257 a 205 c 181 g 242 t

Query Match 32.0%; Score 476.2; DB 10; Length 885;

Best Local Similarity 73.2%; Pred. No. 9.6e-110;

Matches 610; Conservative 0; Mismatches 223; Indels 0; Gaps 0;

Qy 193 CTCAGCTCATGCAGATCATGCGTGGAGAGAACACAGCTTTTAAATACAAACATC 252

Db 885 CTAACACTATGACATATTCGATGTGCAGAGAGATCACTCTTATACGATATT 826

Qy 253 TGGCTTAACTAGAGTGAATGATGAATCTTGGTGGACATCTCAGATTGGCGGG 312

Db 825 TGGCTCAAATGGAATGGAACGATATGAATCTTCGATGAATTCGAGTGAGTTCGGTGT 766

Qy 313 GTCAAAGATTTAAGAGTGCCACCCACACAGCTATGGAACAGAGCTCTTATGACAC 372

Db 765 GTGCGGATCTCGGAATTCGCGACATCGCCTATGGAACCGAGTACTGATGACAC 706

Qy 373 AGCGGGAGGAAGGTTGACAGCAGCTATCAACAGCAGTGTGTGGTGGGAACACGC 432

Db 705 AGTGGCGAGGCTTCGATGGAAGTACGCCACCAATGTGTGTCGAATATGG 646

Qy 433 TCGTGTGTAGTGGCGCGGATCTTCAAGAGCAGCTGGAAGATCGATCACTGG 492

Db 645 AGCTGTCTAGTACCGCAGGTATTTAAGTCAAGTGTGAATGACATTCAGTGG 586

Qy 493 TTCCCTTCGAGCAGCAAGATGCGAGATGAAGTTTGGCAGCTGACATTTATGATGTTAT 552

Db 585 TTCCATTCGAGCAGATGTAATGAAATTTGGTTCGTGGACCTACGATGGGTTT 526

Qy 553 CAGTTGGATCTACAACTACAGGATGAAGGGGCGGAGATATAAGCAGTTTGTACGAAT 612

Db 525 CAGTTGGACCTGACGTCAGGACCAAGTGTGTGGGACATTTCTAGCTTTATACCAAT 466

Qy 613 GCGAATGGAGTTTATAGAGTCCCGGCAAGCGCAAGAGATCTACTACACTGTTGT 672

Db 465 GCGAATGGAGTTTGTAGGTGCGCGGTACTGATCGCTCCATCGCAGCTAGAGGTTTACA 406

Qy 673 CCGGAGCCATACATCGATCAGTTCGGTGTGATCCGAGGAAACGCTCTACTAC 732

Db 405 CAGAACCTTATTTGACATACATTCGCCATTTTGTAAAGGCGCAACGTTGTACTAC 346

Qy 733 TTCTTCAATCTGATCGCTCGCTGCTCATCGCTCCATCGCTCTATTTGGGGTTAC 792

Db 345 TTTTTCATCTGATTTGCGGTGCGTACTGATCGCTCCATCGCAGCTAGAGGTTTACA 286

Qy 793 TTGCTTCAGACTCGGAGAAAAGTTGCTTTTAGTGTGACGATATTACTGCTGAGG 852

Db 285 CTGCCACAGATCTCGGTGAAAAGCTTTTCGCTTGGAGTTTACAAATCTATTATCGCTTACA 226

Qy 853 GTGTTCTCAACATGTCGCGAGAGATGTCAGCAGCTCGGACCGCTGCGCTTGCTC 912

Db 225 GTCTTCTCAACATGTCGCGGAAACAAATGCGCGGACCTCCGATCGCGTACCGCTGCTC 166

Qy 913 GGCACCTACTTCAACTGCATCATGTTTCATGTTGGCTTCTCTCGTGTCCACCATACTG 972

Db 165 GGAACCTATTTCATGTTGATTTATGTTGCTCATCATGTTGTCTCAACCATACTT 106

Qy 973 ATCTCACTACACACCGCGCAGCAGACACTCAGGAATGAGTGTGAT 1025

Db 105 GTCTCAATTATCATCATAGAAATCCAGATACGATGAATGAGTGAATGGT 53

RESULT 2

AL530299

LOCUS

DEFINITION

AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens

CDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.

AL530299

ACCESSION

AL530299.2 GI:31068132

VERSION

EST.

KEYWORDS

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

On Feb 13, 2001 this sequence version replaced gi:12793792.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

7646.r For more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DD007CH030P1&cluster=7646.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ Invitrogen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DD007CH030P1.

Location/Qualifiers

1..1201

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DD007YP05"

/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 258 a 326 c 319 g 273 t 25 others

ORIGIN

Query Match

Best Local Similarity 21.5%; Score 320.6; DB 9; Length 1201;

Matches 564; Conservative 5; Mismatches 360; Indels 11; Gaps 2;

Qy 9 GCGGCGCGCGCTCGCACCTTGGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCT 68

Db 108 GCAGCTCCGGAGCTCAACATGCGTGTGCTGCGGGAGGTTGCTGCTGCGCGCGT 167

Qy 69 CTGCGCGAGGGGGACCGCTGCGGTACACAGAGAGCGGTACTGACACCTATTGGA 128

Db 168 CGCTCCTGACGTGTCCCTGCAAGCGAGTGCAGAGGAAGCTTTTACAAGAGCTG 227

Qy 129 CCACTACACACTGAGAGAGCGCTGCTCAACAGAGCGGCTGCTGCTGCTGCTGCT 188

Db 228 GAACCTACAATCCCTTGGAGAGCGCGGTGGCAATGATCGCAACACCTGCTACTT 287

Qy 189 CGGCTCCTGCTCATGTCAGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 248

Db 288 CTCCTGAGCTCTCTGAGATCATGAGCTGAGTGAAGAGAGAGAGAGAGAGAGAG 347

QY	249	CATCTGGCTAAACCTAGAGTGGAAATGATATGAATCTGAGGTGGAAACACTTTCAGATTTCGG	308
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QY	309	CGGGTCAAGAGTTTAAGATGTCGCCACCCACACAGTATGGAACACAGACGCTCTTATGTA	368
Db	408	AGGGTGAAGACACTGTTGGTTTCCAGATGTCGACATTTTGGAAACACAGACATTTCTCTTA	467
QY	369	CAACAGCGCGGAGGAGGTTGACAGACAGTATCCAAACAGCTGGTGGTGGGAACAA	428
Db	468	TACAGTGGTATGAGCGCTTTGACGCCACATTTCCACATCACTGTTGGTGAATTCCTTC	527
QY	429	CGGCTCGTGTCTGTACGTGCGCCCGGCGCATCTTCAAGAGCACCTGCAAGATCAACATC	488
Db	528	TGGSCATTTGCCAGTWCCTGCTCCAGGCATATTCAAGAGTTCCTGCTACATCATGATGAC	587
QY	489	CTGGTTCCTTCCGACCAACAGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGG	548
Db	588	CTGGTTCCTTCCGACCAACAGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGG	647
QY	549	TTATCAGTTGGATCTCAACATCAGAGTGAAGGGGGGAGATATAGCAGTCTTGTGTCAC	608
Db	648	CTGGTTCCTTCCGACCAACAGATGCGAGATGAAGTTTGGCAGCTGGACTTATGATGG	698
QY	609	GAATGGCGAATGGAGTTAATAGAGTCCCGGCAAGCGCAAGATCTTACTACAAGT	668
Db	699	CAATGGAGATGGACCTAGTGGATCCCGGCAAGAGAGTGAAGGTTCTATGATGATK	758
QY	669	TTGTCGGAGCCATACATCAGATCAGCTTGGTGGTGGTATCGGGAGGAACGCTCTA	728
Db	759	CTGCAAGAGCCCTACCCGATGTCACCTTCCAGATGACATGCGCGGAGGAGCTCTA	818
QY	729	CTACTTCTCAATCTGATGTCGCTCGCTCATCGCTTCCATGCTCTCTATTGGGGTT	788
Db	819	CTATGGCTCAACCTGCTGATCCCTGTGTGCTCACTCCGCTCGCTCGCTGCTGTT	878
QY	789	CACCTTCCTCCAGACTCCGGAG--AAAGTTGCTTTAGTGTGAGATATTACTGTGCG	846
Db	879	CCTGCTTCTGCAAGATTCGCGGGGAGAGATTTCCCTTGGGATACAGATTTACTCTCT	938
QY	847	TTGACGGTGTCTCAACATGTTGGCGGAGACGATCCGACGCTGGAGCGCGTCCCG	906
Db	939	CTTACCGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	998
QY	907	TTGTCGGCAGCTTCTCAACTGATCATGCTTCTGATGTTGGTGG 946	
Db	999	TTGAWAGCCAGTCTTTCGCCAGCACCATCATCATCTGCG 1038	
RESULT 3	AK053497	1864 bp mRNA linear HTC 05-DEC-2002	
LOCUS	DEFINITION	Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched library, clone:E130103E14 product:NEURONAL NICOTINIC ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.	
ACCESSION	VERSION	AK053497.1 GI:26343494	
KEYWORDS	SOURCE	HTC; CAP trapper.	
ORGANISM		Mus musculus (house mouse)	
REFERENCE		Mus musculus	
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.	
TITLE		1	
JOURNAL		Carninci, P. and Hayashizaki, Y.	
MEDLINE		High-efficiency full-length cDNA cloning	
PUBMED		Meth. Enzymol. 303, 19-44 (1999)	
REFERENCE		99279253	
AUTHORS		2	
TITLE		Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
		Normalization and subtraction of cap-trapper-selected cDNAs to	

JOURNAL	prepare full-length cDNA libraries for rapid discovery of new genes
MEDLINE	Genome Res. 10 (10), 1617-1630 (2000)
PUBMED	20499374
REFERENCE	11042159
AUTHORS	3
	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE	20530913
PUBMED	11076861
REFERENCE	4
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seva, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., H., Kontsuki, S. and Hayashizaki, Y.
TITLE	Functional annotation of a full-length mouse cDNA collection
JOURNAL	Nature 409 (6821), 685-690 (2001)
MEDLINE	21085660
PUBMED	11217851
REFERENCE	5
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 1864)
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

4. Kawaji, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kleih, P., Lewis, S., Matsuo, Y., Nikaïdo, I., Pesole, G., Quackenbush, J., Schriber, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Ronaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamlay, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodrigues, I., Sakamoto, N., Sasak, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyokaka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Havash-Shizaki, Y.

Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)

TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2916)

(bases 1 to 10)

Adachi, J., Alzawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawati, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitsu, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Soabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.

Yoshimasa Saito and Hayashizaki, I.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-resgsc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)

cdDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

URL:<http://genome.gsc.riken.go.jp/>
URL:<http://fantom.gsc.riken.go.jp/>

FEATURES

```

I. .2916
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"

```

[illegible]

QY	629	TAGGAGTCCCGGCAAGCGCAACGAGATCTACTACAACCTGTGTCCGGAGCCATACATCG	688
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QY	689	ACATCAACGTTTGGCGTGTGATCCGAGAGAAACGCTACTACTACTTCTTCAATCTGATCG	748
Db	840	ACATCAACGTTTGGCGTGTGATCCGAGAGAAACGCTACTACTACTTCTTCAATCTGATCG	899
QY	749	TGCCCTGGTGTCTATCCGCTCCATCGGCTCTATTGGGCTTCACCTTGCCTCCAGACTCCG	808
Db	900	TTCGCTGCTGCTCATCT	959
QY	809	GAGAAAGTGTCTTTAGTGTGACGATATTAATCTGCTGTTGACGGTGTCTTCAACATCGG	868
Db	960	GGAGAAGGTGACGCTCTGCTATCTCCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1019
QY	869	TGGCGGAGACGATCCGAGCGAGTGGCGGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCT	928
Db	1020	TCACCGAGACCATCCCTTCCACCTCAGTGGTATCCCTTGTATCGGGAGTACCTCCCT	1079
QY	929	GCATCATGTTGATGCTGCT	988
Db	1080	TCACATATGATTTTGTCACTTGTCCATCGTCATCACAGTCTTGTGCTCAACGTGCCT	1139
QY	989	ACCGGACGACGACACTCACGAATGAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT	1048
Db	1140	ACAGAACTCCGACACACACAGATGCCACTTGGTCAAGGCTGTGTTTGAACCTTC	1199
QY	1049	TGCCGTGGTGTGCTGCGCATGTCACGGCC	1076
Db	1200	TCCCCAGGTCATGTTTATGACTAGGCC	1227
RESULT	5		
AK080415			
LOCUS	AK080415	3126 bp mRNA linear HTC 05-DEC-2002	
DEFINITION		Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length	
ACCESSION		enriched library, clone:A730007P14 product:NEURONAL NICOTINIC	
VERSION		ACETYLCHOLINE RECEPTOR ALPHA 3 SUBUNIT, full insert sequence.	
KEYWORDS		AK080415.1 GI:26348538	
SOURCE		HTC; CAP trapper.	
ORGANISM		Mus musculus (house mouse)	
REFERENCE			
AUTHORS		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
TITLE		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
JOURNAL			
MEDLINE		Carninci, P. and Hayashizaki, Y.	
PUBMED		High-efficiency full-length cDNA cloning	
REFERENCE		Meth. Enzymol. 303, 19-44 (1999)	
AUTHORS		99279253	
TITLE		10349636	
JOURNAL			
MEDLINE		Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sasaki, N., Carninci, P.,	
PUBMED		Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.	
REFERENCE		Normalization and subtraction of cap-trapper-selected cDNAs to	
AUTHORS		prepare full-length cDNA libraries for rapid discovery of new genes	
TITLE		Genome Res. 10 (10), 1617-1630 (2000)	
JOURNAL			
MEDLINE		20499374	
PUBMED		11042159	
REFERENCE			
AUTHORS		Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,	
TITLE		Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M.,	
JOURNAL		Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,	
MEDLINE		Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,	
PUBMED		Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,	
REFERENCE		Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,	
AUTHORS		Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
TITLE		RIKEN integrated sequence analysis (RISA) system--384-format	
JOURNAL		sequencing pipeline with 384 multipipillary sequencer	
MEDLINE		Genome Res. 10 (11), 1757-1771 (2000)	
PUBMED		20530913	

11076861	
4	
PUBMED	
REFERENCE	
AUTHORS	
	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
	Arakawa, T., Hara, A., Fushimi, Y., Konno, H., Adachi, J., Fukuda, S.,
	Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I.,
	Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
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	Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N.,
	Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C.,
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	Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohetsuki, S.
	and Hayashizaki, Y.
	Functional annotation of a full-length mouse cDNA collection
	Nature 409 (6821), 685-690 (2001)
	21085660
	11217851
5	
PUBMED	
REFERENCE	
AUTHORS	
	The FANTOM Consortium and the RIKEN Genome Exploration Research
	Group Phase I & II Team.
	Analysis of the mouse transcriptome based on functional annotation
	of 60,770 full-length cDNAs
	Nature 420, 563-573 (2002)
	6 (bases 1 to 3126)
	Fukuda, S., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
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	Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
	Muramatsu, M. and Hayashizaki, Y.
	Direct Submision
	Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
	Physical and Chemical Research (RIKEN), Laboratory for Genome
	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
	RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
	Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp,
	URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
	Fax: 81-45-503-9216)
	cDNA library was prepared and sequenced in Mouse Genome
	Encyclopedia Project of Genome Exploration Research Group in Riken
	Genomic Sciences Center and Genome Science Laboratory in RIKEN.
	Division of Experimental Animal Research in Riken contributed to
	prepare mouse tissues.
	Please visit our web site for further details.
	URL: http://genome.gsc.riken.go.jp/
	URL: http://fantom.gsc.riken.go.jp/.
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DEFINITION	Mus musculus adult male dienecephalon cDNA, RIKEN full-length enriched library, clone:930165116 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.		
ACCESSION	AK034228		
VERSION	AK034228.1	GI:26329798	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci,P. and Hayashizaki,Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2		
AUTHORS	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
REFERENCE	3		
AUTHORS	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakauchi,S., Ikegami,T., Kashiwagi,K., Fujiwara,K., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		
AUTHORS	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamana,I.,		

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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multipillar sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
 20330913
 11076861
 4

REFERENCE

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, F., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660

11217851

REFERENCE

5
 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 Nature 420, 563-573 (2002)

6 (Bases 1 to 3483)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/.

Location/Qualifiers

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ACCESSION

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VERSION

CB149460.1 GI:28132277

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 615)

Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,

Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and

Kim, Y.S.

21C Frontier Korean EST Project 2001

TITLE

Unpublished

JOURNAL

Contact: Kim YS

COMMENT

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Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

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Email: yongsung@mail.kribb.re.kr

Plate: 50 row: D column: 08

High quality sequence stop: 615.

FEATURES

Location/Qualifiers

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intact mRNA was ligated with DNA-RNA linker including

EcoRI site by treatment of T4 RNA ligase and the first

strand cDNA was synthesized from oligo dT-selected mRNA by

priming with dT-tailed vector. The dT-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transfection of

competent cells E. coli Top10F by electroporation method.

The cDNA libraries constructed by this method are

full-length enriched cDNA library."

BASE COUNT 125 a 176 c 155 g 159 t

ORIGIN

Query Match

Best Local Similarity 63.1%; Score 241.4; DB 14; Length 615;

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Db 352 CTATGGCCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCCCTCGCCCTGCTGTT 411
Qy 789 CACCTTGCCTCCAGACTCCCGGAGAAAGTTGTTTGTAGTGTGACGATATTACTTGTGTT 848
Db 412 CTGTCTCTGCGAGATTCGCGGAGAGAGATTTCCTGGGGATTAACAGTCTTACTCTCT 471
Qy 849 GACGGTGTCTCTCAACATGGTGGCGAGACGATGCCAGCGACGTCGGACGCCGTGCCCC 908
Db 472 TACCGTCTTCATGCTGCTGCTGCTGAGATCATGCCCGCAACATCCGATTCGGGTACCAT 531
Qy 909 GCTCGGCACTTACTTCAACTGCAATCATGTTTCATGGTGGCTTCTCCGCTGCTCTCCACC 968
Db 532 GATAGCCCACTACTTCCGCCAGCACCACCATGATCATCGTGGCCCTCTCGGTGGTGGT 591
Qy 969 ACTGATCTCTCAACTTACCACCACC 991
Db 592 GATCGTGTGCGAGTACCACCACC 614

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Search completed: August 21, 2003, 13:12:42

Job time : 3252.96 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2003, 23:54:10 ; Search time 400 Seconds

(without alignments)
10041.909 Million cell updates/sec

Title: US-09-303-232-3_COPY_335_1822

Perfect score: 1488

Sequence: 1 atggcgggcgggcgccgcg.....cgccacacatcatgtgtgcg 1488

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1488	100.0	3700	21	AAZ24476
2	575	38.6	3109	21	AAZ24477
3	512.8	34.5	2886	21	AAZ24475
4	470	31.6	936	23	ABL13733
5	458.2	30.8	1540	23	ABL07231
6	405.6	27.3	1509	22	AAZ90380
7	405.6	27.3	1876	18	AAZ48239
8	405.2	27.2	1876	15	AAV12197

9	405.2	27.2	1876	24	ABV73248	Human neuronal NAC
10	405.2	27.2	1876	24	ABS54875	Human neuronal nic
11	404	27.2	1509	21	AAZ58395	Human PRO2145 nucl
12	404	27.2	1509	22	AAZ90385	Mutant human alpha
13	404	27.2	1509	22	AAZ90386	Mutant human alpha
14	402.4	27.0	1509	22	AAZ90387	Mutant human alpha
15	394	26.5	1590	19	AAV44687	V274T variant huma
16	386.8	26.0	1964	24	ABZ11298	Human polynucleoti
17	327.4	22.0	2769	18	AAZ59196	Neuronal alpha-bun
18	312.2	21.0	2101	18	AAZ59197	Neuronal alpha-bun
19	309.2	20.8	2277	15	AAV12199	Human neuronal nic
20	309.2	20.8	2277	16	AAZ90387	Alpha 2 subunit of
21	309.2	20.8	2277	24	ABV73243	Human neuronal NAC
22	309.2	20.8	2277	24	ABS54870	Human neuronal nic
23	309.2	20.8	2664	18	AAZ48235	Neuronal nicotinic
24	309.2	20.8	2664	24	ABK92165	Prostate cancer-as
25	302.4	20.3	803	23	ABL07799	Drosophila melanog
26	292	19.6	1908	18	AAZ48236	Neuronal nicotinic
27	290	19.5	1416	22	AAZ90382	Chimeric alpha7/5-
28	286.6	19.3	1771	24	AAZ26345	Human mutant neuro
29	286.2	19.2	1809	23	AAZ591552	DNA encoding novel
30	286.2	19.2	2082	18	AAZ59527	Alpha4 subunit of
31	285.2	19.2	1654	24	ABV73244	Human neuronal NAC
32	285.2	19.2	1654	24	ABS54871	Human neuronal nic
33	285.2	19.2	1757	15	AAV12200	Human neuronal nic
34	285	19.2	2448	15	AAZ15343	Human CHRNA2 codin
35	285	19.2	2448	15	AAZ12201	Human neuronal nic
36	285	19.2	2448	18	AAZ48240	Neuronal nicotinic
37	285	19.2	2448	24	ABV73249	Human neuronal NAC
38	285	19.2	2448	24	ABS54876	Human neuronal nic
39	284.6	19.1	2082	18	AAZ59528	Alpha4 subunit of
40	284.6	19.1	3496	18	AAZ48237	Neuronal nicotinic
41	281.8	18.9	1521	12	AAZ14288	Human neuronal nic
42	280	18.8	3649	6	AAZ50416	Calf acetyl cholin
43	275.2	18.5	1667	21	AAZ38821	Human acetylcholin
44	272.8	18.3	1869	24	AAZ45873	Modified acetylcho
45	272.8	18.3	1869	24	ABL54794	Modified hen ACR s

ALIGNMENTS

RESULT 1	AAZ24476
ID	AAZ24476 standard; cDNA to mRNA; 3700 BP.
XX	AAZ24476;
AC	
XX	
DT	17-FEB-2000 (first entry)
XX	
DE	H. virescens acetyl-choline receptor DNA from clone Hva7-1.
XX	
XX	Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
KW	neurotransmission; plant protection agent; conductance; ACHR; ds.
XX	
OS	Heliothis virescens.
XX	
FH	Key Location/Qualifiers
FT	CDS 335..1825
FT	/*tag= a
FT	/product= "acetyl-choline receptor"
XX	
PN	DE19819829-A1.
XX	
PD	11-NOV-1999.
XX	
PF	H. virescens acety
XX	
XX	H. virescens acety
PR	D. melanogaster ac
XX	
PR	Drosophila melanog
XX	
XX	Drosophila melanog
PA	Wild-type human al
XX	
XX	(FARB) BAYER AG.
PI	Adamczewski M, Oellers N, Schulte T;

XX WPI: 2000-014207/02.
 DR P-PSDB; AAY50815.
 XX
 PT New nucleic acid encoding a nicotinic acetylcholine receptor from
 insects, used to identify potential insecticides
 XX
 PS Claim 1a; Page 14-17; 26pp; German.
 XX
 CC This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides, or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence encodes an acetyl-choline
 CC receptor isolated from *Heliothis virescens*.
 XX
 SQ Sequence 3700 BP; 893 A; 953 C; 944 G; 910 T; 0 other;

Query Match 100.08; Score 1488; DB 21; Length 3700;
 Best Local Similarity 100.08; Pred. No. 0;
 Matches 1488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGGGCGGGCGCGCTCGCAGCTTGGCGGCGCGCGGCGCTGCTGCTGCTG 60
 DB 335 ATGGCGGGCGGGCGCGCTCGCAGCTTGGCGGCGCGCGGCGCTGCTGCTGCTG 394
 QY 61 TGCTGCTGCTGCGGAGGGGGGCGCTGCGCTGCTGCGGCTGCGGCTGCTGCTGCTG 120
 DB 395 TGCTGCTGCTGCGGAGGGGGGCGCTGCGCTGCTGCGGCTGCGGCTGCTGCTGCTG 454
 QY 121 CTATGGACCACTACAGCTACTGGAGAGCGCGCTGCTGCTGCGGCTGCGGCTGCTG 180
 DB 455 CTATGGACCACTACAGCTACTGGAGAGCGCGCTGCTGCTGCGGCTGCGGCTGCTG 514
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 DB 515 CTCTCTTGGCGCTGCGGCTGCTGCGGCTGCTGCGGCTGCGGCTGCTGCTGCTGCTG 574
 QY 241 ATAAACAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
 DB 575 ATAAACAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 634
 QY 301 GATTTTCGGCGGGTCAAGATTTAAGAGTGGCCACCCACAGCTATGGAACACGACGTC 360
 DB 635 GATTTTCGGCGGGTCAAGATTTAAGAGTGGCCACCCACAGCTATGGAACACGACGTC 694
 QY 361 CTTATGTACAAACAGCGCGGAGGGTTTCAGACAGCAGTATCCAAACGAGCTGGTGGTG 420
 DB 695 CTTATGTACAAACAGCGCGGAGGGTTTCAGACAGCAGTATCCAAACGAGCTGGTGGTG 754
 QY 421 CGAACAACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
 DB 755 CGAACAACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 814
 QY 481 GACATCACTGTTCCCTTCGACGACCAACAGATGCGAGATGAAGTTTGGCAGCTGGACT 540
 DB 815 GACATCACTGTTCCCTTCGACGACCAACAGATGCGAGATGAAGTTTGGCAGCTGGACT 874
 QY 541 TATGATGTTATCAGTTGGATCTACAACCTACAGGATGAAGGGGGGCGGAGATATAGCAGT 600
 DB 875 TATGATGTTATCAGTTGGATCTACAACCTACAGGATGAAGGGGGGCGGAGATATAGCAGT 934
 QY 601 TTTGTCAGAAATGGGCAATGGAGTTAATAGAGTCCCGGCAACGCAACGAGATCTAC 660
 DB 935 TTTGTCAGAAATGGGCAATGGAGTTAATAGAGTCCCGGCAACGCAACGAGATCTAC 994
 QY 661 TACAACCTGTTGCGGAGCCCATACATCGACATCAGCTTTTGGGTTGCTATCCGGAGGAAA 720

DB 995 TACAACCTGTTGTCGGAGCCCATACATCGACATCATCGTTTGGGTGGTGGTGGTGGTGGT 1054
 QY 721 ACCTCTACTACTTCTTCAATCTGATCGTGCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 780
 DB 1055 ACCTCTACTACTTCTTCAATCTGATCGTGCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1114
 QY 781 TTGGGGTTCACCTTTCCTCCAGACTCCGAGAGAAAGTTGCTTTAGGTGTGACGATATTA 840
 DB 1115 TTGGGGTTCACCTTTCCTCCAGACTCCGAGAGAAAGTTGCTTTAGGTGTGACGATATTA 1174
 QY 841 CTGTCGTGAGGGTGTTCCTCAACATGTTGGCGGAGAGATGCCAGCAGCTCGGACGCC 900
 DB 1175 CTGTCGTGAGGGTGTTCCTCAACATGTTGGCGGAGAGATGCCAGCAGCTCGGACGCC 1234
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 DB 1235 GTGCCCTTGTCTGCGCACCTTCTCAACTGATCATGTTCACTGGTGGTCTTCCCTGCTGCTG 1294
 QY 961 TCCACCATATGATCTCTCAACTACACACCGGACGAGACACTCAGCAATAGTAT 1020
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 QY 1021 TGGATTGCTGCTGCTTCTTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
 DB 1355 TGGATTGCTGCTGCTTCTTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1414
 QY 1081 TCGGCGAGACGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140
 DB 1415 TCGGCGAGACGCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1474
 QY 1141 CGCTCTCAAGTCTGCTAGCGAACTGCTGCGACATCGATCGATGAGGACTTCCGCCACCGG 1200
 DB 1475 CGCTCTCAAGTCTGCTAGCGAACTGCTGCGACATCGATCGATGAGGACTTCCGCCACCGG 1534
 QY 1201 CAAGCGAGACGCGCAATGCTGCGGATACAGGGGGGTGAGGAGAAATGGCGCGGG 1260
 DB 1535 CAAGCGAGACGCGCAATGCTGCGGATACAGGGGGGTGAGGAGAAATGGCGCGGG 1594
 QY 1261 TTGGCGGCGCAGTTGCTTCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1320
 DB 1595 TTGGCGGCGCAGTTGCTTCCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1654
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 DB 1655 AGATCATCAGATCAGATCGGCAAGGACGAGATCGGACATTTCCGGCGACTGG 1714
 QY 1381 AAGTTCCGCGCCATGGTCTGCGACAGACTGTGCTTATTATCTTTACCTCTGTTCAACAATC 1440
 DB 1715 AAGTTCCGCGCCATGGTCTGCGACAGACTGTGCTTATTATCTTTACCTCTGTTCAACAATC 1774
 QY 1441 ATCGCCAGCTAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1488
 DB 1775 ATCGCCAGCTAGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1822

RESULT 2

AAZ24477

ID AAZ24477 standard; cDNA to mRNA; 3109 BP.

XX AC AAZ24477;

XX DT 17-FEB-2000 (first entry)

XX DE H. virescens acetyl-choline receptor DNA from clone Hva7-2.

XX KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;

XX KW neurotransmission; plant protection agent; conductance; AChR; ds.

XX OS Heliothis virescens.

XX PN DE19819829-A1.

XX PD 11-NOV-1999.

XX FH Key Location/Qualifiers
 XX FT CDS 372..2684
 XX FT /*taq= a
 XX FT /product= "acetyl choline receptor."
 XX PN DE19819829-A1.
 XX PD 11-NOV-1999.
 XX PF 04-MAY-1998; 98DE-1019829.
 XX PR 04-MAY-1998; 98DE-1019829.
 XX PA (FARB) BAYER AG.
 XX PI Adamczewski M, Oellers N, Schulte T;
 XX WPI; 2000-014207/02.
 XX DR P-PSDB; AAY50814.
 XX PT New nucleic acid encoding a nicotinic acetylcholine receptor from
 XX PT insects, used to identify potential insecticides
 XX PS Claim 1a; Page 8-12; 26pp; German.
 XX CC This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides, or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence encodes an acetyl-choline
 CC receptor isolated from *Drosophila melanogaster*.
 XX SQ Sequence 2886 BP; 942 A; 687 C; 640 G; 617 T; 0 other;
 Query Match 34.5%; Score 512.8; DB 21; Length 2886;
 Best Local Similarity 62.5%; Pred. No. 5.4e-115;
 Matches 878; Conservative 0; Mismatches 502; Indels 24; Gaps 4;
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 QY 151 CCCGTCGCAACGAGAGCGCCGCTGCAGCTCTCTTCGGCCTCACGCTCATCGAGATC 210
 DB 1356 CCCGTTCTCAATGAATCGGACCCGTTTACAAATTAAGCTTTGGTTTAACTTTAATGCAAAAT 1415
 QY 211 ATCGACGTGGAGGAGAACACGAGCTTTTAAACAAACATCTGGCTAAACACTAGAGTGG 270
 DB 1416 ATCGATGTGGACGAGAAAATCAATGTCTAGTCACTAATGTGTGTTAAACTGGAGTGG 1475
 QY 271 AATGATATGAATCTAGTGTGAACACTTCAGATTTCCGCGGGGTCAAAGATTTAAGAGTG 330
 DB 1476 AACGACATGAATCTCCGCTGGAAACACCTCCGACTATGCGGAGTTAAGGATCTCGGAATA 1535
 QY 331 CCACCCACACACTATGAAACACGAGCTCTTATGTACACACGCGGAGGAGGGTTC 390
 DB 1536 CCGCGCATCGATCTGGAACCGGAGCGTGTGTATGATGATACACAGTGGGAGGATTT 1595
 QY 391 GACAGCAGTATCCAAACGAGCTGGTGTGGGAAACACGCTCGTGTCTGATAGTGGCG 450
 DB 1596 GACGCACTACACACGACGAGCTGGTGTGGGACACGCTCGTGTCTATACGTTCCG 1655
 QY 451 CCGGCGATCTTCAAGAGACGCTGCAAGATCGACATFACCTGCTGCTCCCTTCGACGACAA 510
 DB 1656 CCGGGATCTTCAAGTTCGACGCTGCAAGATCGACATFACCTGCTGCTCCCTTCGATGACCA 1715
 QY 511 CGATCCGAGATGAATTTGGCAGCTGGACTTATGATGTTATCAGTTGATCTACAACTA 570

RESULT 4
 ABL13733
 ID ABL13733 standard; cDNA; 936 BP.
 XX
 AC ABL13733;

Db 1716 CGGTCCGAGATGAAGTTCCGGCAGTTGGACCTACGACGATTCAGCTGGATTCACATTA 1775
 QY 571 CAGGATGAAGGGGGCGAGATATAAGCAGATTTTGTACAGAAATGGGAAATGAGTAAATA 630
 Db 1776 CAAGATGAACACTGGGGGTGATACGAGTTACGTGCTCAACGGGAGTGGGAAGTACTG 1835
 QY 631 GGAGTCCCGGCAAGCGCAACGAGATCTACTACAACTTTGTTCGGAGGCAATACATGAC 690
 Db 1836 GGTGTCCCGGCAAAACGTAACGAGATCTATTACAACTGCTGCCGGAACCTATATAGAC 1895
 QY 691 ATCAGTTTGGGTGGTATCCGGAGGAAAGCTCTACTACTTCTTCAANTGATCGTG 750
 Db 1896 ATCACCCTTCGCCATCATCCGCGGACGACACTGTACTATTCTTCAACTGATCATTA 1955
 QY 751 CCCTGCGTGCATCCGCTCCATGCTATTGGGGTTACCTTGCCTTCCAGACTCCCGGA 810
 Db 1956 CTTGTGTACTGATGCTCCATGCTCCATGCTGCGGATTCACCTGCGCGAGATTCGGGT 2015
 QY 811 GAAAAGTTGCTTTAGTGTGACGATATCTACTGCTGTGAGCGGTGTTCTTCAACATGTTG 870
 Db 2016 GAAAAATTTATCGCTGGGTGTTTACCATCTTGTCTGCTGACCGTGTCTTCTGAATATGTT 2075
 QY 871 GCGGAGACGATCCGACGACGCTCGGACGCGCTGCTTGCCTGCGCACCTACTTCAACATGC 930
 Db 2076 GCCGAGACAATGCCGGCTACTTCCGATCGGTGCCATTG-----TGGATACGC 2123
 QY 931 ATCATGTTTCATGGTGGCTTCTCTCGTCTCTCCACCATACTGATCTTCAACTACACAC 990
 Db 2124 ATCGTGTTTTG--TGCTGGCTGCCATGATATTCCGAATGAGTCGCCCGACGACCGC 2181
 QY 991 CGGACGACGACACTCAGAAATGAGTATGATTTGGATTCGTTGGTGTCTTCTTTATTTGGTG 1050
 Db 2182 TGATCTTAGAGTTCCCGACACGCGCTGTTCCGACACAT---CCTCGAGCGGAAGAC 2237
 QY 1051 CCGTGGTGTGCGCATGTACGCGCGGCTCGGCGACGCGCGCGCGCGCGCGCTA 1110
 Db 2238 CAGATACTCTCGGAGTTGAGCTGAAAGAGCGCTGCTGAAATCGCTGCTGCCAACGTA 2297
 QY 1111 CCTCCGCGCGGACCTGGAGCTGCGGAGCGCTCTCCAAAGTCTCTTACGCAACGTTG 1170
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 Db 2358 CCACACACCCCGGCTTCTATCGCAGCGTTTATGGACAAGGCGAGATGGCAGCATGGG 2417
 QY 1231 TACAGGGGGGTGAGGAGAATGGCGGGGTTGGCGGCGCACAGTTGCTTC-----GGT 1284
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 Db 2478 ACTGAATATGAATAGTTTAACTCTTAAAGGAAATTCGCTTTATAACTGATCAGTACGT 2537
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 QY 1405 AGACTGTCCCTTATTTACTTTTACCTGTTCAAAATCATCGCACCTAGCGCTGCTGCTG 1464
 Db 2598 AGACTGTCCCTTATCATATTACATATTACATGTTTCGAATATTAGCCACAATAGTGTACTACTA 2657
 QY 1465 TCCGCGCACACATCATGTTGTCG 1488
 Db 2658 TCGCACCAACATATTATTGTTCTCG 2681

Db	311	ATGCCAGATTGGAAACAGAGATCTTCTCTATAACAGTGTGATGACGGTTTGACG	370
Qy	395	GCAGTATCAACGAACGCTGGTGGCGGAACAACAGCGTCTGTCTCTACGTGCGCGCCG	454
Db	371	CCACATCCACACTAAGCTGTGGTGAATCTTCTTGGGCATGGCCAGTACTGCTCCAG	430
Qy	455	GCATCTCAAGAGCACCTGCAAGATCGACATCACTGTTTCCCTTCGACGACCAACGAT	514
Db	431	GCATATCAAGAGTTCTCTACATCATGATACGCTGTTTCCCTTTGATGTGCAGCACT	490
Qy	515	GCAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCATGTTGGATCTCAACTACAGG	574
Db	491	GCAACTGAAGTTTGGTCTGTGTTTACGAGGCTGGTCTTGGATCTCGCATGACG	550
Qy	575	ATGAAGGGCGGAGATATAAGCAGTTTGTACGAATGCGAATGGAGTGAATAGGAG	634
Db	551	A-----GGCAGATATCAGTGGCTATATCCCAATGGAGAATGGAGCTAGTGGGAA	601
Qy	635	TCGCCGGAAGCGCAACGAGATCTACTACAACTGTTGTCCGGAGCCATACATCGACATCA	694
Db	602	TCGCCGGAAGAGGAGTGAAGGTTCTATCAGTGTGCAAAAGGCCCTACCCCGATGCA	661
Qy	695	CGTTTGGGTGTGATCCGGAGGAAACGCTCTACTACTTCTCAATCTGATCGTGCCTT	754
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Qy	755	CGGTGCTCATCGCTCCATGCTCTATTGGGTTCACTTGGCTCCAGACTCCGGAGAAA	814
Db	722	GTGTGCTCATCTCGCCCTCGCCCTGCTGGTGTCTTGTCTCTGCAAGATTCGGGGAGA	781
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Db	782	AGATTTCCCTGGGATAACAGTCTTACTCTCTTACCGTCTTCATGCTGCTGTTGCTG	841
Qy	875	AGAGATGCGAAGGACGTCGAGCGCTGCCCTTGTCTGGGACCTACTTCAACTGTCATCA	934
Db	842	AGATCATGCGCGCAACATCGGATTCGGTAGCAATGATAGCCAGTACTTGGCAGCACCA	901
Qy	935	TGTTTCATGGTGGCTTCTCGTGTCTCCACCATACATGATCCTCAACTACCAACCCGCG	994
Db	902	TGATCATCTGTGGGCTCTCGGTGGTGTGACGGTGATCGTGTGCACTACCAACCCACG	961
Qy	995	ACGCAGACACTCACGAATAGTGATGGATTCGTTGCGTGTCTTATTTGGCTGCGCT	1054
Db	962	ACCCGACGGGCAAGATGCCCAAGTGGACAGAGTCACTCTCTGAATGGTGGCGGT	1021
Qy	1055	GGGTGTCGCGATGTCACGCCCGGCTCGCGACGACGCCCGCGCGCGGTACCTC	1114
Db	1022	GGTTCCTGCGAATGAAGAGGCCCGGGAGGACAAAGTGGCGCGCGCTGCGACGACAA	1081
Qy	1115	CGCG-----CCGACCTGGAGCTGCGCGAGCGCTCTCCAAGTCTGCTCTAGCGA	1165
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Qy	1166	ACGTGTCGACATCGATGACGACTTCGCGCACCGCAAGCGACGACGCCCAATGCTGCC	1225
Db	1142	ACGGGAACCTGCTGTACATCGGCTTCGCGGCGCTGGACGGGTGCATGTGTCCGACCC	1201
Qy	1226	GATACTACAGGGGGGTGAGGAGAAATGGCGCGGGTTGGCGGCGACAGTTGTTCCGGT	1285
Db	1202	CCGACTGTGGGTAGTGTGTGGCGCATGGCTGCTCCCGCACGACGATGAGCACCTCC	1261
Qy	1286	TCGACTACGAGCTCTCCCTC-----ATTCTGAAGGAGATTA	1321
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Qy	1322	GAGTCAATCAGATCATGATCGCAAGGACACGAAGATGCGGACATTTCCGGCGACTGGA	1381
Db	1322	GCTACATGCCAATCGCTTCGCTGCCAGACGAAACGAGGCGGTCTGCAGCGAGTGG	1381
Qy	1382	AGTTTCGCCGCATGGTGTGAGACAGACTGTGCCTTATTAATCTTTACCTGTTCAATCA	1441

[illegible]

[illegible]

Db	1262	TGCACGGCGGCAACCCCGGAGGGGAGCCCGGACTTGGCCAAAGATCCTGGAGGAGGTCC	1321
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Db	1322	GCTACATGCCAATCGCTTCGCTGCCAGACGAAACGAGGCGGCTGCAGCGAGTGA	1381
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Db	1382	AGTTTCGCGCGCTGTGTGGTGACGCGCTGTGCCTCATGTGGCTTCTCGGCTCTCACCATCA	1441
Qy	1442	TCGCCACGCTAGCGTCTGCTGTCGCGGCCACACATCATGGTGC	1487
Db	1442	TCTGCACCATCGGCATCCTGATGTCGGCTCCCACTTCGTGGAGGC	1487

RESULT 14
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 ID AAC90387 standard; cDNA; 1509 BP.
 AC AAC90387;
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 XX 14-MAR-2001 (first entry)
 DT
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 XX Mutant human alpha7 ligand gated ion channel coding sequence #3.
 DE
 XX
 KW Human; alpha7 nicotinic acetylcholine gated ion channel; mutant;
 KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200073431-A2.
 XX
 PD 07-DEC-2000.
 XX
 PF 25-MAY-2000; 2000WO-US11862.
 XX
 PR 27-MAY-1999; 99US-0136174.
 XX
 PA (PHAA) PHARMACIA & UPJOHN CO.
 XX
 XX Groppi VE, Wolfe ML, Berkenpas MB;
 PI
 XX WPI; 2001-061524/07.
 XX
 DR P-PSDB; AAB50017.
 DR
 XX
 XX Special cell culture medium for treating cells and for inducing
 PT mammalian cell lines to conduct calcium ions, comprising specified
 PT concentrations of ions of sodium, calcium and potassium at specified pH
 PT
 XX
 XX Claim 64; Page 75; 77pp; English.
 PS
 XX
 XX The present sequence is the coding sequence for a mutant human alpha7
 CC nicotinic acetylcholine gated ion channel. The human alpha7 ion channel
 CC was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)
 CC chimeric ligand gated ion channel (see AAC90382 and AAB50014). The
 CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells
 CC in the present invention, resulting in preferential calcium ion
 CC conductance by the cells. The protein encoded by this sequence has the
 CC wild-type threonine residue at position 230 substituted by a proline
 CC residue and the wild-type cysteine residue at position 241 substituted
 CC by a serine residue.
 XX
 XX Sequence 1509 BP; 297 A; 452 C; 429 G; 331 T; 0 other:

[illegible]

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TITLE Putative alpha subunits of insect nicotinic acetylcholine receptors more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than to other insect nicotinic acetylcholine receptor alpha subunits

JOURNAL

Unpublished

2 (bases 1 to 3629)

Schulte, T., Oellers, N. and Adamczewski, M.

Direct Submission

Submitted (19-APR-1999) ZF-BTB, Bayer AG, Bldg. Q 18., Leverkusen

51368, Germany

FEATURES

Location/Qualifiers

source

1..3629

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BASE COUNT 880 a 931 c 922 g 895 t 1 others

ORIGIN

Query Match 100.0%; Score 1488; DB 3; Length 3629;
Best Local Similarity 100.0%; Pred. No. 6.4e-291;
Matches 1488; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 335 ATGGCGGGCGGGCGGGCGCTGCGCATTGGCGGGCGGGCGGCTGCTGCTGCTG 394
QY 61 TGCCTGCTGCTGCGGCGGGCGGCGCTGCGGGTACACGAGAACGGGCTACTGCAC 120
DB 395 TGCCTGCTGCTGCGGCGGGCGGCGCTGCGGGTACACGAGAACGGGCTACTGCAC 454
QY 121 CTATTGGACCACTACAACTACTGAGAGGCGCGCTGCTCAACGAGAGCGACCGCTG 180
DB 455 CTATTGGACCACTACAACTACTGAGAGGCGCGCTGCTCAACGAGAGCGACCGCTG 514
QY 181 CTCCTCTTGGCGCTCACGCTCATGAGATCATCGACGTGGAGAGAACAGCTTTTA 240
DB 515 CTCCTCTTGGCGCTCACGCTCATGAGATCATCGACGTGGAGAGAACAGCTTTTA 574
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DB 575 ATAACAACATCTGCTAACTAGAGTGAATGATATGAATGAGTGAACACTTCA 634
QY 301 GATTTTGGCGGGTCAAAAGATTAAAGAGTGCCACCCACAGACTATGGAACACGACGTC 360
DB 635 GATTTTGGCGGGTCAAAAGATTAAAGAGTGCCACCCACAGACTATGGAACACGACGTC 694
QY 361 CTTATGTACACAGCGGAGAGGGTTTCGACAGCAGTATCCAAAGACGTGGTGGT 420
DB 695 CTTATGTACACAGCGGAGAGGGTTTCGACAGCAGTATCCAAAGACGTGGTGGT 754
QY 421 CGGAACACGCTGCTGCTGTACGTGCGCGCGCGCATCTTCAAGACACCTGCAGATC 480
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RESULT 2

AX009612

LOCUS

AX009612

DEFINITION

Sequence 3 from Patent Ep0962528.

AX009612

ACCESSION

AX009612.1

GI:9996844

KEYWORDS

linear

DNA

3700 bp

Sequence 3 from Patent Ep0962528.

AX009612

AX009612.1

GI:9996844

KEYWORDS

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LOCUS Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6
DEFINITION subunit variant type I (nAcRalpha-30D) mRNA, complete cds,
alternatively spliced.
ACCESSION AF321445
VERSION AF321445.1 GI:20152844
KEYWORDS Drosophila melanogaster (fruit fly)
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 2023)
AUTHORS Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
TITLE Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
JOURNAL Genetics 160 (4), 1519-1533 (2002)
MEDLINE 21969411
PUBMED 11973307
REFERENCE 2 (bases 1 to 2023)
AUTHORS Grauso, M. and Sattelle, D.B.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
3QX, UK
FEATURES
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1. 2023
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JOURNAL MEDLINE PUBMED REFERENCE AUTHORS JOURNAL FEATURES	RNA-Mediated A-to-I Pre-mRNA Editing Genetics 160 (4), 1519-1533 (2002) 21969411 11973307 2 (bases 1 to 2907) Grauso, M. and Sattelle, D.B. Direct Submission Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU, University of Oxford, South Park Road, Oxford OX1 3QX, UK Location/Qualifiers 1..2907 /organism="Drosophila melanogaster" /mol_type="mRNA" /db_xref="taxon:7227" /chromosome="2" /map="2L: 34E4-5" /dev_stage="embryo" 1..2907 /gene="nAcRalpha-34E" /allele="A" 289..2712 /gene="nAcRalpha-34E" /note="ion channel; neurotransmitter transmembrane receptor" /codon_start=1 /product="nicotinic acetylcholine receptor Dalpha5 subunit" /protein_id="AAM13390.1" /db_xref="GI:20152840" /translation="MKNAQLKLEVDDELWLAVLRHACNSNFSSTRTSSNRH NQLPTLPRLSLTKHNSIAEQHNQOQEPASKDEVDVANHGRSDQOHLQQLDSS NMLSPKTAATAAGDEATTQOPTNIRLCARKRQLRRRRKRPATNETDIKQOOL SMPPKRTSDTYSTPAATSCPTATYMOCRASDNFSIPISRHDVSTATFAWLH VLOVLLSKOOWLHVQOVSLLFPRTAASTIAFISYLSGFAALKNSSSSSSNSS NNSQTILGNLKHSHFELLYLNLAKVCLAGVHEKRLDLDLPYNTLERPVNLN DPLQSLGLILMQLIDVDEKNOLLVNWLNKLEWDMNLRWNTSDYGVXDLRLPBR IWKPDVLYNSADGDFGTGTNNVVRNNGSLVPPGIFKSKIDITWFPFDDQRC EMKFSYTGFDQLDQDETGGDISYVLNGEWELGVPGRNELYNCPEPYID ITFAIIIRRTLYFFNLIIPCVLIASMAILGFTLPDPSGKLSLGYTILLSLTVFLN MVAETPATSDAVPLLGTYENCIMFWASSVSVTILILNYHHRNADTHSEWIRIVF LCWLPIRLMSRGRPLLEPPTPCSDTSERKHOILSDVELKERSKSLLANVLDI DDDRHRCRPMWPGTILPHNPAFYRTYVGDDGSGIPGSTRMPDAVTHHTCKSST EYELGLILKEIRFTIDOLRKDDCEDIANWKFAAMVVDRLCLLIIFTMFAILLATIAVL LSAPHIIVS" 373 /gene="nAcRalpha-34E" /note="compared to B allele" /replace="a" 375 /gene="nAcRalpha-34E" /note="results in phenylalanine to isoleucine substitution; compared to B allele" /replace="c" 827 /gene="nAcRalpha-34E" /note="results in threonine to isoleucine substitution; compared to B allele" /replace="t" 1079..1080 /gene="nAcRalpha-34E" /note="results in lysine to arginine substitution; compared to B allele" /replace="g" 1081..1086 /gene="nAcRalpha-34E" /note="results in deletion of asparagine and serine; compared to B allele" /replace="" 1119~1120 /gene="nAcRalpha-34E" /note="results in serine, glycine, and asparagine insertion; compared to B allele" /replace="accqcaac"	variation 1121 /gene="nAcRalpha-34E" /note="results in asparagine to serine substitution; compared to B allele" /replace="g" BASE COUNT 935 a 696 c 642 g 634 t ORIGIN Query Match 39.2%; Score 583.8; DB 3; Length 2907; Best Local Similarity 65.2%; Pred. No. 7.le-108; Matches 976; Conservative 0; Mismatches 422; Indels 99; Gaps 4; QY 91 GGGTACCACGAGAGAGCGGTACTGCACCACTATTGGACCACTACAAGTACTGGAGAGG 150 DB 1213 GGATATCATGAAAAGAGAGACTGTACACGATCTTTTGGATCTTATAATACATAGAAGCT 1272 QY 151 CCCGTCGTCAAGGAGAGAGCGCCCTGCAGCTCTCTTCGGCCCTCAGCTCATCAGATC 210 DB 1273 CCCGTTCTCAATGAATCGGACCCCTTACAAATTAAGCTTTGGTTTAACTTTAATGCAAAAT 1332 QY 211 ATCGACGTGGACGAGAAGAACACAGCTTTTATAACAACAACATCTGGCTAAACACTAGAGTGG 270 DB 1333 ATCGATGTGGACGAGAAAATCAATTCGTACTCACTAATGTGTGTGTTAAACACTGAGTGG 1392 QY 271 AATGATATGAACATTGAGTGGACACTTCAGATTTCCGGGGGTCAAGATTTAAGAGTG 330 DB 1393 AACGACATGAATCTCCGCTGGACACCTCCGACTATGGCGAGTTAAGGATCTCGGAATA 1452 QY 331 CCACCCACAGACTATGAAACACAGAGCTCTTATGTACACACGCGGAGAGAGGCTTC 390 DB 1453 CCGCGGCATCGCATCTGGAAGCGGAGCTGTGTATGTACACAGCTGGGATGAGGGAATTT 1512 QY 391 GACACGACGATTCACAAACGACGCTGGTGGCGGAACAACGCTGCTGTCTGTACGTCCG 450 DB 1513 GACGCGACCTACCAGACAGAGCTGGTGGTGGCGGAACAACGCTGCTGTCTATACGTTCG 1572 QY 451 CCGCGCATCTTCAAGAGACACTTCAAGATCGACATCACTGCTGGTTCCTTCGACGACAA 510 DB 1573 CCGGGGATCTTCAAGTCAAGCTGCAAGATCGACATCACTGCTGGTTCCTTCGATGACGAG 1632 QY 511 CGATCCGAGATGAAGTTTGGCAGCTGACATATCATGTTATCATGTTTGGATCTCAACTA 570 DB 1633 CGGTGCGAGATGAAGTTTCGGCAGTTGGACCTACACAGGATTTCCAGCTGGATTTACAATTA 1692 QY 571 CAGGATGAAGGGCGGAGATATAAGCAGATTTTGTTCACGAAATGGGAGTTAATA 630 DB 1693 CAAGATGAACCTGCGGTGATATCAGCAGTTACGTGCTCAACGCGAGTGGGAACTACTG 1752 QY 631 GGAGTCCCGCAAGCGCAACGAGATCTACTACAACCTGTTGTCGGAGCCATACATCGAC 690 DB 1753 GGTGTGCCCGCAAAACGTAACGAGATCTATTACAACCTGCTCCCGGAAACCTATATAGAC 1812 QY 691 ATCAGCTTTGGGTGGTGTATCCGAGGAAACGCTCTACTACTTCTTCAATCTGATCGTG 750 DB 1813 ATCAGCTTCGGCATCATCTCCGCGGACGACACTGTACTATTTCTTCAACCTGATCATA 1872 QY 751 CCCTCGGTGCTCATCGCTCCATCGCTCTATTGGGGTTCACTTCCCTCCAGACTCCGGA 810 DB 1873 CCTTGTGCTAGATTGCTTCCATCGCTTGTCTCGGATTCACCTTCCCGCCAGATTCGGGT 1932 QY 811 GAAAAAGTTGCTTTAGTGTGACGATATTAATGCTGTTGACGGGTGTTCTCTCAACATGGTG 870 DB 1933 GAAAAATTAATCGTGGGTGTTACCATCTTGTCTCTCGCTGACCGGTGTTCTTGAATATGTT 1992 QY 871 GCGGAGAGATGCCAGCAGCTGCGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930 DB 1993 GCCGAGACAATGCCGGCTACTTCCGATGCGGTGCGCATTTGCTGGGTACATATTTCAATTCG 2052 QY 931 ATCATGTTTCATGGTGGCTTCCCTCGCTGCTCTCCACCATCTGATCTCTCAACTACACCCAC 990 DB 2053 ATAAATGTTTATGGTAGCTTTCATCCGTTGTGTCAACAGATTTTAAATATTAAATATCATCAT 2112 QY 991 CGGCACGACAGACTCAGGAAATGAGTATGATTCGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1050
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Qy 1286 -----TCGACTAGAGCTCTCCCTCATCTG 1311
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Db 2533 AAGGAATTCGCTTAACTGATCAGTACGTAAGATGACGAGTGCATGATGATGATGCC 2592
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RESULT 9
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LOCUS Heliothis virescens putative nicotinic acetylcholine receptor alpha
DEFINITION 7-2 subunit mRNA, complete cds.
ACCESSION AF143847
VERSION AF143847.1 GI:4895006
KEYWORDS Heliothis virescens (tobacco budworm)
SOURCE Heliothis virescens
ORGANISM Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
REFERENCE 1 (bases 1 to 3029)
AUTHORS Schulte,T., Oellers,N. and Adamczewski,M.
TITLE Putative alpha subunits of insect nicotinic acetylcholine receptors
more similar to vertebrate alpha 7 subunits and C. elegans Ce21
than to other insect nicotinic acetylcholine receptor alpha
subunits
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3029)
AUTHORS Schulte,T., Oellers,N. and Adamczewski,M.
TITLE Direct Submission
JOURNAL Submitted (19-APR-1999) 2F-BTB, Bayer AG, Bldg. Q 18,, Leverkusen
51368, Germany
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Best Local Similarity 64.6%; Pred. No. 4.3e-106;
Matches 929; Conservative 0; Mismatches 460; Indels 48; Gaps 3;
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RESULT 10
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
source
CDS

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 AX009614.1 GI:9996846
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 Noctuoidea; Noctuidae; Heliothinae; Heliothis.
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 Adamczewski,M.D., Schulte,T.D. and Oellers,N.D.
 Nucleic acids encoding acetylcholin-receptor subunits from insects
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LOCUS E58348 3109 bp DNA linear PAT 18-JUN-2001
DEFINITION Nucleic acid encoding insect acetyl choline receptor subunit.
ACCESSION E58348
VERSION E58348.1 GI:13019347
KEYWORDS JP 2000023680-A/3.
SOURCE Heliothis virescens (tobacco budworm)
ORGANISM Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
REFERENCE 1 (bases 1 to 3109)
AUTHORS Martin,A., Nadjia,E. and Thomas,S.
TITLE Nucleic acid encoding insect acetyl choline receptor subunit
JOURNAL Patent: JP 2000023680-A 3 25-JAN-2000;
BAYER AG
COMMENT OS Heliothis virescens
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PF 26-APR-1999 JP 1999118159
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ORIGIN
Query Match 38.6%; Score 575; DB 6; Length 3109;
Best Local Similarity 64.6%; Pred. No. 4.3e-106;
Matches 929; Conservative 0; Mismatches 460; Indels 48; Gaps 3;
QY 97 CACGAGAAGCGGTACTGACACCTATTTGGACACCTATACAACTGACTTGGAGAGCCCGTC 156
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VERSION	AF321449		
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ORGANISM	Drosophila melanogaster		
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AUTHORS	1 (bases 1 to 2110)		
TITLE	Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.		
JOURNAL	Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing		
MEDLINE	Genetics 160 (4), 1519-1533 (2002)		
PUBMED	21969411		
REFERENCE	11973307		
AUTHORS	2 (bases 1 to 2110)		
TITLE	Grauso, M. and Sattelle, D.B.		
JOURNAL	Direct Submission		
FEATURES	Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OX1 30X, UK		
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DB 50/ GCTGGAGCGACCCGCTGGCCCAATGAATCGGAGCCCCCTGGAGGTTAAGTTCGGACTGACGCT 566

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QY 381 CGAAGGGTTCGACAGCACGTATCCAACGGAACGTGGTGGTCCGGAACAACGGGCTCGTGCTT 440

A vertical ruler with a dashed line on the left and a solid line on the right. The ruler is marked with centimeters from 0 to 10. The 0 mark is at the top, and the 10 mark is at the bottom. The ruler is oriented vertically.

Db 747 TGAGGGATTTCGATGGCAGTATCACACCAACATTGTGGTCAAACATAACGGCAGTTGTCT 806

Qy	441	GTACGTCCGCGCGGCAATCTTCAAGAGCACCCTGCAAGATCGCATCACCTGGTTCCCTTT	500
Db	807	GTACGTCCCCCTGGTATCTTCAAGAGCACATGCAAGATGGACATCACGTGGTTCCCAT	866
Qy	501	CGACGCAACGATCGAGATGAAGTTTGGCAGCTGGACTTATGATGGTTATCAGTTGGA	560
Db	867	TGATGACCAACATTCGGAATGAATTCGGTAGTTGGACTTACGATGGAAATCAGTTGGA	926
Qy	561	TCTACAACACTACAGGATGAAGGGGCGGAGATATAAGCAGTTTGTCCAGAAATGGCAATG	620
Db	927	TTTGTTTGAATTCGGAAGATGGAGGATCTTCCGATTTTCATAACAATGGCGAGTG	986
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Qy	681	ATACATCGACATCACGTTTCGGTGGTGATCCGGAGAAACCTCTACTACTTCTTCAA	740
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Qy	741	TCTGATCGTGCCTCGCTGCTCATCGCCTCCATGGCTTATTTGGGGTTCACCTTGGCTCC	800
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Qy	801	AGACTCGGAGAAAAGTTGTCTTTAGGTGTGACGATATTAATCTCGTTGACGGTGTCT	860
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Qy	861	CAACATGGTGGCGAGAGATGCCAGGAGTCCGAGCGG-----	901
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Qy	902	-----	901
Db	1287	AATTCCTTATCGCTCACAGTGTTCCTCAACCTTTGTAGCTGAGACATTGCCCAAGTATC	1346
Qy	902	-----TGCCCTTGTGCGGCACTTCTCACTACATGCATCAATGTTCAATGGTGTTCCTC	953
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Qy	954	CGTCTCTCCACCATACTGATCTCACTACCAACCGCAGCAGACACTCACCAAT	1013
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Qy	1014	GAGTGATTTGATTCGTTTCCTTTATTTGGCTGCCCTGGGTCTCGCATGTCGACG	1073
Db	1467	GCCACGTGATCAAGTCCGTTTTCCTACAAATGGCTGCCCTGGATCTTGGAAATGGTGC	1526
Qy	1074	GCCGGCTCGGAGACAGCGCGCGCGCGCGGTAC---CTCCGCGCGGACCTGGA	1130
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Qy	1131	GCTCGCGAGCGTCTCCAAAGTCGCTCTAGCGAAAGTCTCGACATCGATCAGCACATTT	1190
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Qy	1191	CCGCGCAACGCAAGCGCAGCGCAATGCTGCCGATACTACAGGGGGGTGAGAGAA	1250
Db	1647	TCGGCACACAATATCTGGCTCCCAACCGCCATTGGCTCGTGGCCAGCTTCGGTCGGC	1706
Qy	1251	TGGCGCGGGTTGGCGGCGCACAGTTGCTTTCGGTGTGCTGACTAC---GAGCTCTCCCTCAT	1307
Db	1707	CACAACGTTGGAGGAGCATCACACGGCCATTCGGCTGCAATCACAAAGATCTTCATCTAAT	1766
Qy	1308	TCTGAAGGAGATTAGATCATCAGATCAGATGCCAAGGACGACGAGATCGCGACAT	1367
Db	1767	TCTTAAAGAAATGCAATTTATTCGCGCGGATTCGCAAAAGCTGACGACGAAACGGAAT	1826
Qy	1368	TTGCGGAGCTGGAAGTTCCCGCCATGGTTCGTGGACAGACTGTGCTTTATTATCTTTAC	1427
Db	1827	GATCGGCGATTGGAAGTTCCGGCAATGGTGTGGATAGATTTTGTTTAATGTTTTCAC	1886
Qy	1428	CCTGTTCCACAATCATGCCACGCTAGCCGTTGCTGCTCGCGGCCACACATCATGTGTG	1485

Db	1887	GCCTCTACGATTATTGCAACGGTTACGGTGCTGCTCTCGCTCCGCACATAATCGNG	1944
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AX009610			
LOCUS	AX009610	2886 bp	DNA linear PAT 06-SEP-2000
DEFINITION	Sequence 1 from Patent EP0962528.		
ACCESSION	AX009610		
VERSION	AX009610.1	GI:9996842	
KEYWORDS			
SOURCE	Drosophila melanogaster (fruit fly)		
ORGANISM	Drosophila melanogaster		
REFERENCE	Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidae; Drosophilidae; Drosophila.		
AUTHORS	Adamczewski, M.D., Schulte, T.D. and Oellers, N.D.		
TITLE	Nucleic acids encoding acetylcholin-receptor subunits from insects		
JOURNAL	Patent: EP 0962528-A 1 08-DEC-1999;		
FEATURES	BAYER AG (DE)		
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	/db_xref="taxon:7227"		
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	/note="unnamed protein product"		
	/codon_start=1		
	/protein_id="CAC07499.1"		
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BASE COUNT	942 a 687 c 640 g 617 t		
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	Best Local Similarity 62.5%; Pred. No. 1.7e-93;		
	Matches 878; Conservative 0; Mismatches 502; Indels 24; Gaps 4;		
QY	91	GGGTACCAGAGAAGCGGTACTGCACCACTATTGGACCACTACACGTTACTGGAGAGG	150
Db	1296	GGATATCATGAAAGAGACTGTTACACGACTCTTTGGATCTCTTATATACACTAGAACGT	1355
QY	151	CCGCTGCTCAACGAGAGCGACCGCTGCAGCTCTCTTCGGCCCTCAGCTCATCAGATC	210
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QY	211	ATCGAGCTGGACGAGAAGACAGCTTTTATAACAAACATCTGGCTAAAACCTAGAGTGG	270
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QY	271	AATGATATGAATCTGAGGTGGAACTTCAGATTCGGCGGGGTCAAGATTTAAGAGTG	330
Db	1476	AACGACATGAATCTCGCTGGAAACACCTCCGACTATGGCGGAGTTAAGGATCTCGGAATA	1535
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QY	391	GACAGCAGCTATCCAACGACAGCTGGTGGTGGCGGAACAAACGGCTGTGCTGTACGTCCG	450

Db 2658 TCGGACCACATATTATGTCG 2681

Search completed: August 21, 2003, 09:54:17
Job time : 5551.39 secs

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	Score	Match	Length			
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2	1191.5	29.5	502	3	US-08-464-238B-7	Sequence 7, Appli
3	1191.5	29.5	502	3	US-08-471-961-7	Sequence 7, Appli
4	1168	28.9	511	1	US-08-278-635B-8	Sequence 8, Appli
5	1168	28.9	511	3	US-08-464-258B-8	Sequence 8, Appli
6	1168	28.9	511	3	US-08-471-961-8	Sequence 8, Appli
7	1159.5	28.7	502	2	US-08-466-589-8	Sequence 8, Appli
8	1159.5	28.7	502	2	US-08-700-636-8	Sequence 8, Appli
9	1159.5	28.7	502	3	US-08-467-574-8	Sequence 8, Appli
10	1159.5	28.7	502	4	US-09-217-345-8	Sequence 8, Appli
11	1159.5	28.7	502	4	US-08-487-536-12	Sequence 12, Appli
12	1155.5	28.6	502	4	US-08-771-737-2	Sequence 2, Appli
13	848.5	21.0	529	1	US-08-496-855A-2	Sequence 2, Appli
14	848.5	21.0	529	4	US-08-487-536-2	Sequence 2, Appli
15	848.5	21.0	529	4	US-08-660-451A-2	Sequence 2, Appli
16	845	20.9	504	4	US-08-660-451A-4	Sequence 2, Appli
17	835	20.7	528	2	US-08-466-589-2	Sequence 2, Appli
18	835	20.7	528	2	US-08-700-636-2	Sequence 2, Appli
19	835	20.7	528	3	US-08-467-574-2	Sequence 2, Appli
20	835	20.7	528	4	US-09-217-345-2	Sequence 2, Appli
21	832.5	20.6	510	1	US-08-278-635B-4	Sequence 4, Appli
22	832.5	20.6	510	3	US-08-471-961-4	Sequence 4, Appli
23	827	20.5	511	3	US-08-464-258B-4	Sequence 4, Appli
24	823.5	20.4	497	1	US-08-278-635B-5	Sequence 5, Appli
25	823.5	20.4	497	3	US-08-464-238B-5	Sequence 5, Appli
26	823.5	20.4	497	3	US-08-471-961-5	Sequence 5, Appli
27	810	20.0	504	2	US-08-466-589-4	Sequence 4, Appli

APPLICATION NUMBER: US/08/471,961
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/278,635
FILING DATE: 21-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 502 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-471-961-7

Query Match 29.5%; Score 1191.5; DB 3; Length 502;
Best Local Similarity 46.0%; Pred. No. 4.3e-107;
Matches 240; Conservative 80; Mismatches 117; Indels 85; Gaps 10;
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DB 8 IWLALAAALLHVSLOGEFORRLKELVKNYPLERPVPANDSQPLTVFVLSLLQINDVDE 67
QY 354 KNQLLVNTWKLWMDNLRWNTSDYGGVKDLRIHPHRIWKPDVLMYNSADGFGTGYQ 413
DB 68 KNQVLATNIWLQSWTDHYLQNMNSEYPGKYNRFPDQGIWKPDILLYNSADRFDAFTH 127
QY 414 TNVVRNNGSLVYPPGIFKSTCKIDITWPFDDQCEMFGSWTVDGFDLOLODETG 473
DB 128 TNVLVNASGHQVLPFGIFKSSCYIDVRWPFDDVQCKLKFGSWSGWSLQMQE--- 184
QY 474 GDTSVYVNGEWELLGVPGKRNEIYNCCEPYIDITFAIIRRTLYYFFNLIIPCVLI 533
DB 185 ADISSYIPNGEWDLMGIPGKRNEKYECCKEPYDPVTYVTMRRTLYYGLNLLIPCVLI 244
QY 534 ASWALLGFTLPPSGEKLISGLVTLLSLTVFLNVAETMPATSDAVPL----- 581
DB 245 SALALLVFLLPADSGEKISGLVTLLSLTVFLNVAETMPATSDVPLIAQYFASTMIIV 304
QY 582 -----WIRIVFLCWLPMILRMSRP-----RPLILEPTTP 612
DB 305 GLSVVTVIVLYRHHDPDGGKMPKWTIRIILLNCAWFLRMKRPGEKVKRPACQKRP-RP 363
QY 613 CSOTSSERKHQILSDVELKERSKSLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRTV 672
DB 364 CS-----LASVELSAG-----PPTSGNLLY--IGFRGL 392
QY 673 YGO-----GDDGSI-GPIGSTRMPDAVTHHTCIKSSTEYELGILKEIRITOLKRDDE 726
DB 393 EGMHCAPTDSGVYCGRLACSPTHDEHLMHGAHPSDGDPDLAKILEEVRYIANRFRQDE 452
QY 727 CNDIANDKFAAMVDRCLIIIFTMFAILATIAVLLSAPHII 768
DB 453 SEVICSEWKPACVDRCLMAFSVFTICTIGILMSAPNFV 494

RESULT 4
US-08-278-635B-8
Sequence 8, Application US/08278635B
Patent No. 5683912
GENERAL INFORMATION:
APPLICANT: ELGOYHEN, ANA BELEN
APPLICANT: JOHNSON, DAVID S.
APPLICANT: BOULTER, JAMES R.
APPLICANT: HEINEMANN, STEPHEN F.
TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: GRAY CARY WARE & FREIDENRICH
STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/278,635B
FILING DATE: 21-JUL-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9771
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-677-1409
TELEFAX: 619-677-1465
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 511 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-278-635B-8
Query Match 28.9%; Score 1168; DB 1; Length 511;
Best Local Similarity 44.2%; Pred. No. 8.5e-105;
Matches 238; Conservative 83; Mismatches 117; Indels 100; Gaps 12;
QY 285 NGUNKHSWIFLLIYLNLSAKVCLAGYHEKRLHLDLPYNTLERPVNLSDPQLQSLFGLT 344
DB 12 SGLCLWASLFSF-----KVSQOQESQRRLYDLRNRYNLRLEPVMNDSQPIVVELQLS 66
QY 345 LMOIIDDEKNOLLVTNWLKLEWMDNLRWNTSDYGGVKDLRIHPHRIWKPDVLMYNSA 404
DB 67 LLGIIDVDEKNQVLITNWLQMTWVDIYLSNDQYEPGVQNLNRPDSQIWPDIILYNSA 126
QY 405 DEGDGTQYTNVVRNNGSLVYPPGIFKSTCKIDITWPFDDQCEMFGSWTVDGFDQ 464
DB 127 DEREDATEFTNLVNVYSGSQYIPPGILKSTCYIDVRWPFDDVQCKLKFGSWTHSGWLI 186
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QY 525 NLIIPCVLASMALGFTLPPDSDGEKISGLVTLLSLTVFLNVAETMPATSDAVPL--- 581
DB 244 NLLIPCVLISGLALLVFLLPADSGEKISGLVTLLSLTVFLNVAETMPATSDVPLIAQ 303
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DB 304 YFASIMVIVGLSVVTVIVLQFHHDHPQAGKMPRWVRVILLNCAWFLRMKPGENIKPL 363
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DB 388 QPSGNNMIYSYHTMENPCCPNNDLGSKSKITCPLSED--NEHVOKKALMDTIPVVKI 445
QY 711 LKEIRFITDOLRRKDDCNDIANDKFAAMVDRCLIIIFTMFAILATIAVLLSAPHII 768
DB 446 LEEVQFIAMFRKQDEGEIEICSEWKFAAVDRCLVAFITLFAICTFTILMSAPNFI 503

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RESULT 5
US-08-464-258B-8
; Sequence 8, Application US/08464258B
; Patent No. 6013766
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH LLP
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,258B
; FILING DATE: 06/05/95
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9989
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-464-258B-8

Query Match 28.9%; Score 1168; DB 3; Length 511;
Best Local Similarity 44.2%; Pred. No. 8.5e-105;
Matches 238; Conservative 83; Mismatches 117; Indels 100; Gaps 12;

QY 285 NGLNKHSTWFLIYLNLSAKVCLAGYHEKRLHLDLPYNTLERPVNLSDPQLSFGILT 344
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QY 405 DEGFDTGTQTVNVRNNGSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOL 464
Db 127 DERFDTFTNVLNVNGSCQYIPGILKSTCYIDVRWPFDDVQKDLKFGSWTHSGWLI 186
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Db 187 DLQMLE---ADISNYISNGEWDLVGPGRNELYECCKEPYDPVTTYITMRRRLTYXGL 243
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Db 244 NLLIPCVLISGALLVFLLPADSGEKISGLITVLLSLTVFLMLVAEIMPATSDSVPLIAQ 303
QY 582 -----WIRIVFLCWLPMILRMSRPG---RPL 604
Db 304 YFASIMVIVGLSVVVTVLVLPQHHDPQAGKMPRWVRVILLNWCWFLRMKFGGENIKPL 363

QY 605 ILEFPTTPCSDTSSERKHQILSDVELKERSKSLANVLDIDDDFRHNCRPMTPGGTILPH 664
Db 364 SCKY-----SYPKHPSLKNTEM-----NVL-----PG-----H 387
QY 665 NPAFYRTVYG-----QGDD--GSIGPIGSTRMPDAVTHHTCIKS--STEYELGLI 710
Db 388 QPSNGNMIYSYHTMENPCQPONNDIGSKSGKITCPLSED--NEHVQKKALMDTIPVIVKI 445
QY 711 LKEIRFITDOLRKDDCNDIANDMKFAAMVWVDRCLLIIFTMFAILATIAVLLSAPHII 768
Db 446 LEEVQFTIAMRFRKQDEGEICESEKFAAAVDRCLCLVAFITFAICTTILMSAPNFI 503

RESULT 6
US-08-471-961-8
; Sequence 8, Application US/08471961
; Patent No. 6100046
; GENERAL INFORMATION:
; APPLICANT: ELGOYHEN, ANA BELEN
; APPLICANT: JOHNSON, DAVID S.
; APPLICANT: BOULTER, JAMES R.
; APPLICANT: HEINEMANN, STEPHEN F.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF A NOVEL
; TITLE OF INVENTION: ACETYLCHOLINE-GATED ION CHANNEL RECEPTOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GRAY CARY WARE & FREIDENRICH
; STREET: 4365 EXECUTIVE DRIVE, SUITE 1600
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,961
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/278,635
; FILING DATE: 21-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: REITER, STEPHEN E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9771
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-677-1409
; TELEFAX: 619-677-1465
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 511 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-471-961-8

Query Match 28.9%; Score 1168; DB 3; Length 511;
Best Local Similarity 44.2%; Pred. No. 8.5e-105;
Matches 238; Conservative 83; Mismatches 117; Indels 100; Gaps 12;

QY 285 NGLNKHSTWFLIYLNLSAKVCLAGYHEKRLHLDLPYNTLERPVNLSDPQLSFGILT 344
Db 12 SGCLWASLFLSFF-----KVSQGESQRRYDLLRNRLRPMVNDSPQIVVELQLS 66
QY 345 LMQIIDVDKKNOLLVTNVWKLWMDNMLRWNTSDYGGVKDLRIPIPHRIWKPDVLYNSA 404
Db 67 LLIQIIDVDKKNOLLVTNVWKLWMDNMLRWNTSDYGGVKDLRIPIPHRIWKPDVLYNSA 126
QY 405 DEGFDTGTQTVNVRNNGSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOL 464
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Db 127 DERFATHTNVLVNYSGSCQIPPGILKSTCYIDVRWEPFDVQKCDLKFSGWTHSGWLI 186
QY 465 DILOQDETGGDTSYVNGEWELLVGPGKRNELIYNCCPEPYDITFAIIIRRTLYYFF 524
Db 187 DILOME---ADISNYSINGEWDLVGPGRNELIYECCKEPYDVTYITMRRRLYYGL 243
QY 525 NLIIPCVLIASMLLGFLLPPDPSGKLSIGVTLLSLTVFLNNVAETMPATSDAVPL--- 581
Db 244 NLLIPCVLISGLALLVFLPADSGEKISIGITVLLSLTVFLLVAELMPATSDSVPLIAQ 303
QY 582 -----WIRIVFLCWLPPWILRMSRPG---RPL 604
Db 304 YFASIMVIVGLSVVTVLVQLFHHDPQAGKPRVVRVILLNWCAMFLRMKKGKGENIKPL 363
QY 605 ILEFPTTSCDTSSEKHKHOLLSDVELKRSKSLLANVLDDIDDFRHNCRPMTPGTGLPH 664
Db 364 SKY-----SYPKHPSLKNTEM-----NVL-----PG-----H 387
QY 665 NPAFYRTVYG-----QGDD--GSIGPIGSTRMPDAVTHHTCIKS--STEYELGLI 710
Db 388 QPSNGNMIIYHTMENPCQPQNNDLGSKSKITCPLSED--NEHVQKKALMDTIPVIVKI 445
QY 711 LKEIRITDQLRKDDCNDCIANDKFAAMVVDRLCLIIFTMFAILATIIVLSAPHII 768
Db 446 LEEVQFIAMFRKQDEGEICSEWKFAAVAIDRLCLVAFLEFAIITCTFTILMSAPNFI 503

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RESULT 7

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US-08-466-589-8
; Sequence 8, Application US/08466589
; Patent No. 5837489
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L.
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 502 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

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US-08-466-589-8

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Query Match 28.7%; Score 1159.5; DB 2; Length 502;
Best Local Similarity 45.1%; Pred. No. 5.6e-104;
Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;
QY 297 IYLNLSAK---YCLAGYHEKRLHLLDLPYNTLERPVNLNESDPLQSLFGLTLMQIDVDE 353
Db 8 VMLAASLLHVSLOGEFORKLYKELVKNYNPLERPANDSOPLTVYFSLSLQIQMDVDE 67
QY 354 KNQLLTVNWLEWDMNLRWNTSDYGGVKDLRIPPHRIKWPDLVYNASDEGDTYQ 413
Db 68 KNOVLTITNLQMSMTDHYLQNVSEYPGKVTFRPDGOIQMKPDLILLYNSADEREDATEPH 127
QY 414 TNVVRNNGSCLYVPGPIFKSTCKIDITWFPDDQRCENKFGSWTVDGFLQDLQLODETG 473
Db 128 TNVLYNSSGHCOYLPPGIFKSSCYIDVRWFEDVQHKLKFSGWSYGGWSLDLOMQE--- 184
QY 474 GDISSYVLNGEWELLVGPGKRNELIYNCCPEPYDITFAIIIRRTLYYFFNLIIPCULI 533
Db 185 ADISGYPNGEWDLVGIPGKRSERFECCKEPYDVTFTVTRRRRTLYYGLNLLIPCVLI 244
QY 534 ASMALGFTLPDPSGKLSIGVTLLSLTVFLNNVAETMPATSDAVPL----- 581
Db 245 SALALLVFLPADSGEKISIGITVLLSLTVFLLVAELMPATSDSVPLIAQFASTMIIV 304
QY 582 -----WIRIVFLCWLPPWILRMSRPG---RPLLEPPTTP 612
Db 305 GLSVVTVIVLQYHHHDPDGGKMPKTRVILLNWCAMFLRMKRGEDKVRP-ACQHKORR 363
QY 613 CSDTSERKHQILSDVELKERSKSLLANVLDDIDDFRH-----NCRPMTPGTGLPHNPAF 668
Db 364 CSLASVE-----MSAVAPPPASGNLLY-----IGFRGLDGVHCV-TP----- 401
QY 669 YRTVYGGDGSIGPIGSTRMPDAVTH-----HTCIKSSSTEYELGLILKEIRITDQLRK 723
Db 402 -----DSGVV-----CGMACSPHDEHLHGQPPGDPDLAKILEEVRIANRFR 449
QY 724 DDECNDIANDKFAAMVVDRLCLIIFTMFAILATIIVLSAPHII 768
Db 450 QDESEAVCSEWKFACVVDRLCLMAFSVTIICTIGILMSAPNFV 494

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RESULT 8

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US-08-700-636-8
; Sequence 8, Application US/08700636
; Patent No. 5910582
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,636
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993

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[illegible]

TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-487-596-12

Query Match 28.7%; Score 1159.5; DB 4; Length 502;
Best Local Similarity 45.1%; Pred. No. 5.6e-104;
Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;
Db 8 VWLALASLLHVSLOGEQRKLYKELVKNYNPLERPVANDSOPLTVEYFSLQIMQDVE 67
QY 297 IYLNLSAK---VCLAGYHEKRLHLLDPYNTLPERVNLNESDPLQSLFGLTLMQIDYDE 353
QY 354 KQNLVTVNWKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPVDVLMYNSADEGPDGYQ 413
Db 68 KQNLVTVNWKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPVDVLMYNSADEGPDGYQ 413
QY 414 TNVVRNNGSLYVPPGIFKSTCKIDITWFFPDQORCEMKFGSWTYDGFOLDLQLODETG 473
Db 128 TNVVRNNGSLYVPPGIFKSTCKIDITWFFPDQORCEMKFGSWTYDGFOLDLQLODETG 473
QY 474 GDISYVLNGWELLGVPGKRNIEYNCPEPYIDITFAIIRRTLYFFNLIIPCVLI 533
Db 185 ADISYIPNGEWDLVGIPGKRSERYECKEPEYDVTFTVMRRRTLYGLNLLIPCVLI 244
QY 534 ASMLLGTLPDPSGEKLSGLVITLLSVTLVFNVAETMPATSDAVPL----- 581
Db 245 SALALLVLLPADSGEKISLGITVLLSLTFTVLLVAEIMPATSDSVPLIAQYFASMTIIV 304
QY 582 -----WIRIVFLCWLPLWILRMSRPG-----RPLILEFPTTP 612
Db 305 GLSVVTVTVILOYHHDDPGGKMPKWTIVILLNWCANFLMKRPGEDKVRP-ACQHKORR 363
QY 613 CSDTSSERKHQILSDVELKRSKSLANVLDIDDDFRH-----NCRPMTPGTGLPHNPAF 668
Db 364 CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCV-TP----- 401
QY 669 YRTVYGGDDGSGIGSTRMPDATH-----HTCIKSTVEYELGLILKEIRFITDQLRK 723
Db 402 -----DSGVV-----CGRMACSPTHDEHLLHGQPPGDPDLAKILLEEVRIANRRC 449
QY 724 DDECNDIANDKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
Db 450 QDESEAVCEWKFACVVDRLCLMAFSVTIICTIGILMSAPNFV 494

RESULT 12
US-08-771-737-2

; Sequence 2, Application US/08771737
; Patent No. 6323000
; GENERAL INFORMATION:
; APPLICANT: Briggs, Clark A.
; APPLICANT: Gopalakrishnan, Murali
; APPLICANT: McKenna, David G.
; APPLICANT: Monteggia, Lisa M.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Sullivan, James P.
; APPLICANT: Touma, Edward
; APPLICANT: Abbott Laboratories
; TITLE OF INVENTION: A VARIANT HUMAN ALPHA 7 ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR SUBUNIT, AND METHODS OF PRODUCTION AND USES THEREOF
; FILE REFERENCE: 6017 US 01
; CURRENT APPLICATION NUMBER: US/08/771,737
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRF
; ORGANISM: homo sapien
US-08-771-737-2
Query Match 28.6%; Score 1155.5; DB 4; Length 502;
Best Local Similarity 45.0%; Pred. No. 1.4e-103;

Matches 236; Conservative 82; Mismatches 116; Indels 91; Gaps 12;
QY 297 IYLNLSAK---VCLAGYHEKRLHLLDPYNTLPERVNLNESDPLQSLFGLTLMQIDYDE 353
Db 8 VWLALASLLHVSLOGEQRKLYKELVKNYNPLERPVANDSOPLTVEYFSLQIMQDVE 67
QY 354 KQNLVTVNWKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPVDVLMYNSADEGPDGYQ 413
Db 68 KQNLVTVNWKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPVDVLMYNSADEGPDGYQ 413
QY 414 TNVVRNNGSLYVPPGIFKSTCKIDITWFFPDQORCEMKFGSWTYDGFOLDLQLODETG 473
Db 128 TNVVRNNGSLYVPPGIFKSTCKIDITWFFPDQORCEMKFGSWTYDGFOLDLQLODETG 473
QY 474 GDISYVLNGWELLGVPGKRNIEYNCPEPYIDITFAIIRRTLYFFNLIIPCVLI 533
Db 185 ADISYIPNGEWDLVGIPGKRSERYECKEPEYDVTFTVMRRRTLYGLNLLIPCVLI 244
QY 534 ASMLLGTLPDPSGEKLSGLVITLLSVTLVFNVAETMPATSDAVPL----- 581
Db 245 SALALLVLLPADSGEKISLGITVLLSLTFTVLLVAEIMPATSDSVPLIAQYFASMTIIV 304
QY 582 -----WIRIVFLCWLPLWILRMSRPG-----RPLILEFPTTP 612
Db 305 GLSVVTVTVILOYHHDDPGGKMPKWTIVILLNWCANFLMKRPGEDKVRP-ACQHKORR 363
QY 613 CSDTSSERKHQILSDVELKRSKSLANVLDIDDDFRH-----NCRPMTPGTGLPHNPAF 668
Db 364 CSLASVE-----MSAVAPPPASNGNLLY-----IGFRGLDGVHCV-TP----- 401
QY 669 YRTVYGGDDGSGIGSTRMPDATH-----HTCIKSTVEYELGLILKEIRFITDQLRK 723
Db 402 -----DSGVV-----CGRMACSPTHDEHLLHGQPPGDPDLAKILLEEVRIANRRC 449
QY 724 DDECNDIANDKFAAMVVDRLCLIIFTMFAILATIAVLLSAPHII 768
Db 450 QDESEAVCEWKFACVVDRLCLMAFSVTIICTIGILMSAPNFV 494

RESULT 13

US-08-496-855A-2
; Sequence 2, Application US/08496855A
; Patent No. 5801232
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; Zip: 92101-2926
; COMPUTER-READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,855A
; FILING DATE: 20-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie

REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-9369B
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-238-0999
 TELEFAX: 619-238-0062
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 529 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-496-855A-2

Query Match 21.0%; Score 848.5; DB 1; Length 529;

Best Local Similarity 36.7%; Pred. No. 1.1e-73;

Matches 183; Conservative 87; Mismatches 154; Indels 75; Gaps 10;

QY 309 GYH---EKRLHLLDLPYNTLERPVNLNESDPLSGLTLMLQIIDVDKRNQLLVTVNLWK 365
 Db 53 GSHTETEDRLFKHLFRGYNRWARPVPTSDVIVRFGLSIAQLIDVDKRNQMTTNWLK 112
 QY 366 LEWDMNLRNWTSDYGVKDLRIPPHRIKPDVLMYNSADEGFDGTQYQTNVVRNNGSCL 425
 Db 113 QEWSDYKLRNPNADFGNITSLRVPSEMIWIPDIVLYNNADGEFAVTHMTKAHLFSTGTVH 172
 QY 426 YVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFQDLQDQDETGGDISSYVLNGEW 485
 Db 173 WVPPIAYKSSCSIDVTFFPDDQCNCKMKFGSWTYDKAKIDLEQMEQT-VDLKDYWESGEW 231
 QY 486 ELGVPKGRNEIYNNCCPEYIDITFAIIRRTLYFFNLIIPCVLIASMLLGTLP 545
 Db 232 AIVNATGTYNSKKYDCAEYIPDVTYAFVIRRLPLEYTNLIIPCLLSCLTVLVFPLS 291
 QY 546 DSGEKLSLGVITLLSITVFLNMVAETMPATSDAVPL----- 581
 Db 292 DCGEKITCLISVLLSTVFLNLTETIIPSTSLVPLIGEYLLFTMFVLSIVITVFLN 351
 QY 582 -----WIRIVLCWLPWILRMSRPGRLILEPTTPCSDTSERKHQILSDV 628
 Db 352 VHRSPSTHTMPHWRGALLGCVPRWLLMNRPPPPVEL---CHPLRLKLSPSYHWLESNV 408
 QY 629 ELKERSKSLANVLIDDDFRNCR-PMTPG-GTLPHPAFYRTVYGGDDSGSIGPGS 686
 Db 409 DAEERE-----VVVEEDRWACAGHAPSVGTL-----CSHGLHSGASGPKAE 452
 QY 687 TRMPDA---VTHHTCIKSSTEYELGLILKEIRITDOLRKDDCNDIANDKFAAMVDR 743
 Db 453 ALLQEGELLSPH-----MOKALEGVHIAHLRSEDADSSVKEDWKYVAMVIDR 502
 QY 744 LCLIIFTMFALATIIVALL 762
 Db 503 IFLWLFIIVCFGLGTIGLFL 521

RESULT 14

US-08-487-596-2

Sequence 2, Application US/08487596

Patent No. 6440681

GENERAL INFORMATION:

APPLICANT: Elliot, Kathryn J.

APPLICANT: Ellis, Steven B.

APPLICANT: Harpold, Michael M.

TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND

TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL

TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McClain

STREET: 1660 Union Street

CITY: San Diego

STATE: CA

COUNTRY: USA

ZIP: 92101

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,596
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO US94/02447
 FILING DATE: 08-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/149,503
 FILING DATE: 08-NOV-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/028,031
 FILING DATE: 08-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/938,154
 FILING DATE: 30-NOV-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/504,455
 FILING DATE: 03-APR-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Seidman, Stephanie L.
 REGISTRATION NUMBER: 33,779
 REFERENCE/DOCKET NUMBER: 6362-9951
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-238-0999
 TELEFAX: 619-238-0062
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 529 amino acids
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-487-596-2

Query Match 21.0%; Score 848.5; DB 4; Length 529;

Best Local Similarity 36.7%; Pred. No. 1.1e-73;

Matches 183; Conservative 87; Mismatches 154; Indels 75; Gaps 10;

QY 309 GYH---EKRLHLLDLPYNTLERPVNLNESDPLSGLTLMLQIIDVDKRNQLLVTVNLWK 365
 Db 53 GSHTETEDRLFKHLFRGYNRWARPVPTSDVIVRFGLSIAQLIDVDKRNQMTTNWLK 112
 QY 366 LEWDMNLRNWTSDYGVKDLRIPPHRIKPDVLMYNSADEGFDGTQYQTNVVRNNGSCL 425
 Db 113 QEWSDYKLRNPNADFGNITSLRVPSEMIWIPDIVLYNNADGEFAVTHMTKAHLFSTGTVH 172
 QY 426 YVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFQDLQDQDETGGDISSYVLNGEW 485
 Db 173 WVPPIAYKSSCSIDVTFFPDDQCNCKMKFGSWTYDKAKIDLEQMEQT-VDLKDYWESGEW 231
 QY 486 ELGVPKGRNEIYNNCCPEYIDITFAIIRRTLYFFNLIIPCVLIASMLLGTLP 545
 Db 232 AIVNATGTYNSKKYDCAEYIPDVTYAFVIRRLPLEYTNLIIPCLLSCLTVLVFPLS 291
 QY 546 DSGEKLSLGVITLLSITVFLNMVAETMPATSDAVPL----- 581
 Db 292 DCGEKITCLISVLLSTVFLNLTETIIPSTSLVPLIGEYLLFTMFVLSIVITVFLN 351
 QY 582 -----WIRIVLCWLPWILRMSRPGRLILEPTTPCSDTSERKHQILSDV 628
 Db 352 VHRSPSTHTMPHWRGALLGCVPRWLLMNRPPPPVEL---CHPLRLKLSPSYHWLESNV 408
 QY 629 ELKERSKSLANVLIDDDFRNCR-PMTPG-GTLPHPAFYRTVYGGDDSGSIGPGS 686
 Db 409 DAEERE-----VVVEEDRWACAGHAPSVGTL-----CSHGLHSGASGPKAE 452
 QY 687 TRMPDA---VTHHTCIKSSTEYELGLILKEIRITDOLRKDDCNDIANDKFAAMVDR 743

Db 453 ALLQEGELLSPH-----MOKALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDR 502

QY 744 LCLIIFTMFATIAVL 762

Db 503 IFLWLFIIIVCFGLTGFL 521

RESULT 15

US-08-660-451A-2
; Sequence 2, Application US/08660451A
; Patent No. 6524789
; GENERAL INFORMATION:
; APPLICANT: Elliott, Kathryn J.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,451A
; FILING DATE: June 7, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/484,722
; FILING DATE: 06/07/95
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9370B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 529 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-660-451A-2

Query Match 21.0%; Score 848.5; DB 4; Length 529;
Best Local Similarity 36.7%; Pred. No. 1.1e-73;
Matches 183; Conservative 87; Mismatches 154; Indels 75; Gaps 10;
QY 309 GYH---EKRLHDLDPYNTLPRVNESDPLQLSFGLTLMQIIDVDEKNQLLVNWLK 365
Db 53 GSHTETEDLFLKPLRGYNRWARPVNTSDVVIVRFGLSIAQLIDVDEKNQMMTTNVWLK 112
QY 366 LEWDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMNSADEGFGDGTOTNVVVRNNGSCL 425
Db 113 QEWSYKLRWNPADFGNTISLRVSEMIWIPDIVLYNNRADGEFATHMTKALHFTGTGVH 172
QY 426 YVPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGFQDLQLODETGGDISSYVYNGEW 485
Db 173 WYPPAIYKSSCSIDYTFEFPDQCNCKMKFGSWTYDKAKIDLQEQMT-VDLKDYWESGEW 231

QY 486 ELLGVPGKRNEIYNCCPEPIDITFAIIIRRTIYYFENLIIPCVLIASMLLGTLP 545
Db 232 AIVNATGYNSKKYDCCAEIYPDVYAFVIRRLPLFTYINLIIPCLLSCLTVLVYLP 291
QY 546 DSGEKLSLGVTTLLSLTVFLANVAETMPATSDAVPL----- 581
Db 292 DCGEKITLCISVLLSLTVFLLLITELIIFSTLSVILPGLCEYLLFTWIFVTL 351
QY 582 -----WIRIVFLCWLPMILRMSRPGRLILEFFPTPCSDTSSERKHQILSDV 628
Db 352 VHRSPSTHTPHWVRGALLGCVPRWLLMNRPPVPEL---CHPLRLKLSPSYHWLESNV 408
QY 629 ELKERSKSLANVLDDIDDDFRHNCR-PMTPG-GTLPHNPAPYRVYGGDDSGSGPG 686
Db 409 DAEERE-----VVVEEDRWACAGHVAPSVGTL-----CSHGHLHSGASGPKAE 452
QY 687 TRMPDA---VTHHTCIKSTVEYELGLILKEIRFITDQKDDCEDNDIAWKAAMVVD 743
Db 453 ALLQEGELLSPH-----MOKALEGVHYIADHLRSEDADSSVKEDWKYVAMVIDR 502
QY 744 LCLIIFTMFATIAVL 762
Db 503 IFLWLFIIIVCFGLTGFL 521

Search completed: August 13, 2003, 15:43:09
Job time : 25.5314 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:20 ; Search time 73.6446 Seconds
(without alignments)
2698.100 Million cell updates/sec

Title: US-09-303-232-2
Perfect score: 4043
Sequence: 1 MKNQLKLTVEVDDDELMLAV.....MFALATIAVLVSAPHIIVS 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4014.5	99.3	807	5 Q8T7V5	Q8T7V5 drosophila
2	2388.5	59.1	482	5 Q8T5P5	Q8T5P5 drosophila
3	1988	49.2	545	5 Q9VW19	Q9VW19 drosophila
4	1850	45.8	496	5 Q9XZ13	Q9XZ13 drosophila
5	1625.5	40.2	494	5 Q8T7S2	Q8T7S2 drosophila
6	1622.5	40.1	494	5 Q8T7S3	Q8T7S3 drosophila
7	1620.5	40.1	494	5 Q8T7S1	Q8T7S1 drosophila
8	1611	39.8	523	5 Q8T7R9	Q8T7R9 drosophila
9	1609	39.8	501	5 Q9XZ14	Q9XZ14 heliothis v
10	1502	39.6	509	5 Q8T7S0	Q8T7S0 drosophila
11	1502	37.2	391	5 Q9NKD2	Q9NKD2 drosophila
12	1310.5	32.4	554	5 Q9V179	Q9V179 drosophila
13	1235	30.5	525	5 Q8IPE2	Q8IPE2 drosophila
14	1186	29.3	273	5 Q9VJT9	Q9VJT9 drosophila
15	1185.5	29.3	502	11 Q9JHD6	Q9JHD6 mus musculus
16	1168	28.9	511	13 Q03481	Q03481 gallus gall

17	1140	28.2	335	5 Q9NKD1	Q9NKD1 drosophila
18	1015	25.1	480	5 Q8I932	Q8I932 caenorhabdi
19	1009.5	25.0	461	5 P91197	P91197 caenorhabdi
20	977	24.2	554	5 Q62083	Q62083 caenorhabdi
21	968.5	24.0	542	5 Q18556	Q18556 caenorhabdi
22	902	22.3	537	5 Q8MUR0	Q8MUR0 apis mellif
23	897	22.2	515	5 Q46133	Q46133 locusta mig
24	888.5	22.0	537	5 Q9U941	Q9U941 myzus persi
25	888	22.0	567	5 Q9VC74	Q9VC74 drosophila
26	883.5	21.9	523	5 Q46128	Q46128 heliothis v
27	882.5	21.8	552	5 P91765	P91765 myzus persi
28	876	21.7	568	5 Q9NFR5	Q9NFR5 drosophila
29	875	21.6	545	5 Q96631	Q96631 heliothis v
30	861.5	21.3	531	5 Q96632	Q96632 heliothis v
31	859	21.2	536	5 Q8T0Y9	Q8T0Y9 alysia cal
32	854	21.1	540	5 Q46134	Q46134 locusta mig
33	854	21.1	595	5 P91764	P91764 myzus persi
34	851	21.0	509	5 Q9NFX8	Q9NFX8 myzus persi
35	849	21.0	497	5 Q46135	Q46135 locusta mig
36	849	21.0	509	5 Q8MM21	Q8MM21 aphid gossy
37	847.5	21.0	512	11 Q91X60	Q91X60 mus musculu
38	843	20.9	533	5 Q8WRS1	Q8WRS1 chilo suppr
39	843	20.9	536	5 Q8T9S0	Q8T9S0 alysia cal
40	840	20.8	783	5 Q9W366	Q9W366 drosophila
41	839	20.8	559	5 Q46132	Q46132 locusta mig
42	837	20.7	517	5 Q96633	Q96633 heliothis v
43	833	20.6	795	5 Q18394	Q18394 drosophila
44	829.5	20.5	219	5 Q8T5F4	Q8T5F4 drosophila
45	827.5	20.5	499	11 Q8VHH6	Q8VHH6 mus musculu

ALIGNMENTS

RESULT 1

Q8T7V5	PRELIMINARY;	PRT;	807 AA.
ID	Q8T7V5;		
AC	Q8T7V5;		
DT	01-JUN-2002 (Tremblrel. 21, Created)		
DT	01-JUN-2002 (Tremblrel. 21, Last sequence update)		
DT	01-MAR-2003 (Tremblrel. 23, Last annotation update)		
DE	Nicotinic acetylcholine receptor Dalp5a5 subunit.		
GN	NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR CG4498 OR CG16878.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21969411; PubMed=11973307;		
RA	Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;		
RT	"Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalp5a5, Dalp5a6 and Dalp5a7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing.";		
RT	Genetics 160:1519-1533(2002).		
RL	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.		
CC	EMBL; AF272778; AAM13390.1; -		
DR	FlyBase; FBgn0028875; nACR-alpha-34E.		
DR	InterPro; IPR006201; Neur_chan.		
DR	InterPro; IPR006202; Neur_chan_LBD.		
DR	InterPro; IPR006029; Neu_channel_memb.		
DR	Pfam; PF02931; Neur_chan_LBD; 1.		
DR	Pfam; PF02932; Neur_chan_memb; 1.		
DR	TIGRfams; TIGR00860; Lic; 1.		
DR	PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.		
KW	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;		
KW	Transmembrane.		
SEQUENCE	807 AA; 91223 MW; C8B4F6B34287C8C8 CRC64;		

Query Match	99.3%	Score	4014.5	DB	5	Length	807
Best local Similarity	95.4%	Pred.	No. 0				
Matches	770	Conservative	0	Mismatches	0	Indels	37
Gaps	1						
QY	1	MKNAQLKLT	EVDDDELAVRLAHCSNFS	SSSSSTRITSSNORINQOOLT	TLQPSLSLTKH	60	
DB	1	MKNAQLKLT	EVDDDELAVRLAHCSNFS	SSSSSTRITSSNORINQOOLT	TLQPSLSLTKH	60	
QY	61	HSNIASQHN	SQQEPASKDEVDVANHGSRNDQO	THLQOLDSSNMLSPKTAATAAAGDEA	120		
DB	61	HSNIASQHN	SQQEPASKDEVDVANHGSRNDQO	THLQOLDSSNMLSPKTAATAAAGDEA	120		
QY	121	TTQOPTNIR	LCAKRBQLRRRRKKPATPNET	DIKKOQOLSMPFKRKSDTDTSTPAAT	180		
DB	121	TTQOPTNIR	LCAKRBQLRRRRKKPATPNET	DIKKOQOLSMPFKRKSDTDTSTPAAT	180		
QY	181	TSOPTATY	MOCRASDNFSPISRHRVSYATFAW	LHVQLVLSQOOWLHVQOORSVL	240		
DB	181	TSOPTATY	MOCRASDNFSPISRHRVSYATFAW	LHVQLVLSQOOWLHVQOORSVL	240		
QY	241	LFRRIAST	TAFTSYLGSFAQLKNSSSSSSSNS	STQIILNGLNKHSWIFLLIYN	300		
DB	241	LFRRIAST	TAFTSYLGSFAQLKNSSSSSSSNS	STQIILNGLNKHSWIFLLIYN	300		
QY	301	LSAKVCLAG	YHEKRLLDHLLDPYNTL	LRPVLNESDPLQLSFGLTLMQI	IDVDENKQLLVT	360	
DB	301	LSAKVCLAG	YHEKRLLDHLLDPYNTL	LRPVLNESDPLQLSFGLTLMQI	IDVDENKQLLVT	360	
QY	361	NVWLKLEW	NDMLRWNTSDYGGVKDLRIP	PHRIWKPDVLMYNSADEGFGTYQT	NVVVRN	420	
DB	361	NVWLKLEW	NDMLRWNTSDYGGVKDLRIP	PHRIWKPDVLMYNSADEGFGTYQT	NVVVRN	420	
QY	421	NGSCLYPP	GGIFKSTCKIDITWFPDDO	RCMKFGSWTYDGFOLDLOLQDET	GDISSY	480	
DB	421	NGSCLYPP	GGIFKSTCKIDITWFPDDO	RCMKFGSWTYDGFOLDLOLQDET	GDISSY	480	
QY	481	INGEWELL	GVPGKREIYINCCPEPYIDIT	FAIIRRTLYFFENLIIPCVL	IASMALLG	540	
DB	481	INGEWELL	GVPGKREIYINCCPEPYIDIT	FAIIRRTLYFFENLIIPCVL	IASMALLG	540	
QY	541	FTLPDPSG	EKLSLGVTTLLSLTVPLN	MAETMPATSDAVPL-----	581		
DB	541	FTLPDPSG	EKLSLGVTTLLSLTVPLN	MAETMPATSDAVPL-----	581		
QY	582	-----	-----	-----	-----	581	
DB	582	-----	-----	-----	-----	581	
QY	601	ILILNYH	RNRADTHEMSEWIRIVEL	WLPWLIRMSRPGRLILEFPT	PCSDTSERKHQ	660	
DB	601	ILILNYH	RNRADTHEMSEWIRIVEL	WLPWLIRMSRPGRLILEFPT	PCSDTSERKHQ	660	
QY	624	ILSDVELK	ERSKSLLANVLIDDDFR	HNCRPMTPGGTLP	HPNPAFYRTVYQGDDGSIGP	683	
DB	661	ILSDVELK	ERSKSLLANVLIDDDFR	HNCRPMTPGGTLP	HPNPAFYRTVYQGDDGSIGP	720	
QY	684	IGSTRMP	DVATHHTCIKSSEYE	LGILLKEIRFTTDOL	KDKDECNDANKKFAAMVYDR	743	
DB	721	IGSTRMP	DVATHHTCIKSSEYE	LGILLKEIRFTTDOL	KDKDECNDANKKFAAMVYDR	780	
QY	744	LCLIFTM	FAIATIAVLLSAPHI	IVS	770		
DB	781	LCLIFTM	FAIATIAVLLSAPHI	IVS	807		

[illegible]

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OC NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21959411; PubMed=11973307;
RX Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalpha5, Dalpha6 and Dalpalpha7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AY036613; AAK67256.1; "
DR FlyBase; FBGN0028875; nAcr-alpha-34E.
DR InterPro; IPR006201; Neur_channel.
DR InterPro; IPR006202; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 482 AA; 54445 MW; A4B95B921CA33F05 CRC64;

Query Match 59.18; Score 2388.5; DB.5; Length 482;
Best Local Similarity 98.3%; Pred. No. 1.6e-197;
Matches 457; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

Qy	1	MKNAQLKLTVEVDDDELWAVLRAHC	SNFSSSSSTRITSSNQRHNQOLTTLOPRLSTK	60
Db	1	MKNAQLKLTVEVDDDELWAVLRAHC	SNISSSSTRITSSNQRHNQOLTTLOPRLSTK	60
Qy	61	HSNIASBOHNSQOQEPASKDEVDVANHG	RSNDQOQTHLOQDSSNMLSPKTAAATAAGDEA	120
Db	61	HSNIASBOHNSQOQEPASKDEVDVANHG	RSNDQOQTHLOQDSSNMLSPKTAAATAAGDEA	120
Qy	121	TTQOPTNIRLCARKRQRLRRRRKKRPAT	PNETDIKKOQQLSMPFPKTKKSTDYTSPTAAT	180
Db	121	TTQOPTNIRLCARKRQRLRRRRKKRPAT	PNETDIKKOQQLSMPFPKTKKSTDYTSPTAAI	180
Qy	181	TSOPTATYMOCRASDNFEFSPISRHDRV	STATFAWLHVLOQLVLSLQOQWLHVQOORSVL	240
Db	181	TSOPTATYMOCRASDNFEFSPISRHDRV	STATFAWLHVLOQLVLSLQOQWLHVQOORSVL	240
Qy	241	LFERRIAASTIAFTSYLGSFAQLKNS	SSSSSSSSSSNSTQILNGLNKHWSIFLLIYL	299
Db	241	LFERRIAASTIAFTSYLGSFAQLR	SSSSSSSSSSNSTQILNGLNKHWSIFLLIYL	300
Qy	300	NLSAKVCLAGYHEKRLHLDDLDPYNT	LTERPVINESDPLQLSFGLTLMQIIDVDEKNQLLV	359
Db	301	NLSAKVCLAGYHEKRLHLDDLDPYNT	LTERPVINESDPLQLSFGLTLMQIIDVDEKNQLLV	360
Qy	360	TNWLKLEWMDMNLRWNTSDYGGVKDL	RIPPHRTWKPDVLMYNSADEGFGDGTYTQNVVVR	419
Db	361	TNWLKLEWMDMNLRWNTSDYGGVKDL	RIPPHRTWKPDVLMYNSADEGFGDGTYTQNVVVR	420
Qy	420	NNGSCLVYVPGIFKSTCKIDITWPFDD	QDQCEMKFGSWTYDGFOL	464
Db	421	NNGSCLVYVPGIFKSTCKIDITWPFDD	QDQCEMKFGSWTYDGFOL	465

RESULT 3	
Q9VMW19	
ID	PRELIMINARY; PRT; 545 AA.
AC	Q9VMW19;
DC	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE	CG32538 protein.
GN	NACR-ALPHA-18C OR CG8082 OR CG8109 OR CG32538.
OS	Drosophila melanogaster (Fruit fly).
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_TaxID=7227;
 RP [1]
 RC SEQUENCE FROM N.A.
 RX STRAIN=Berkeley.
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Anantides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandal M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Folsler K., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang S., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Anantides P.G., Brandon R.C., Rogers Y.,
 RA Banon J., An H., Baldwin D., Banon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacieb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Swirkas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RA "Sequencing of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradscky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RA "Annotation of Drosophila melanogaster genome";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]

RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003511; AAF48950.2;
 DR FlyBase; FBgn0031014; nACR-alpha-18C.
 DR InterPro; IPR006201; Neur_channel.
 DR InterPro; IPR006202; Neur_channel_LBD.
 DR InterPro; IPR006029; Neur_channel_memb.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRFASTS; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 SQ SEQUENCE 545 AA; 61517 MW; 7B83025107A66209 CRC64;
 Query Match 49.2%; Score 1988; DB 5; Length 545;
 Best Local Similarity 71.0%; Pred. No. 7.3e-163;
 Matches 384; Conservative 46; Mismatches 51; Indels 60; Gaps 8;
 QY 276 SNNSTQILNKLKSHWIFLLIYLNLSAKVCLAGYHEKRLHLLDLPYNTLERPVNESD 335
 DB 15 SANCANSON-----IVOSVLMELVFHSCAAGPEKRLHLLDLPYNTLERPVNESD 65
 QY 336 PLQSLSGTLMLQIIVDEKQNLVTVNWLKLENDMLRWNTSDYGVKDLRIPPHRIWK 395
 DB 66 PLQSLSGTLMLQIIVDEKQNLVTVNWLKLENDMLRWNTSDYGVKDLRIPPHRIWK 125
 QY 396 PDVLMYNSADEGFGTYQTNNVVRNNGSCLYVPPGIFKSTCKIDITWFPDDQRCMKFG 455
 DB 126 PDVLMYNSADEGFGTYQTNNVVRNNGSCLYVPPGIFKSTCKIDITWFPDDQRCMKFG 185
 QY 456 SWTYDFQDLQLODETGDISYVNLNGEWELLGVPKRNEIYNNCCPEYIDITFAILL 515
 DB 186 SWTYDFQDLQLODETGDISYVNLNGEWELLGVPKRNEIYNNCCPEYIDITFAILL 245
 QY 516 RRTLYFFNLIIPCVLIASMAILGFTLPDPDSGEKLSGLVTILLSLTVFLNMVAETMPAT 575
 DB 246 RRTLYFFNLIIPCVLIASMAILGFTLPDPDSGEKLSGLVTILLSLTVFLNMVAETMPAT 305
 QY 576 SDAVPL-----WIRVFLCWLPIWLRMS 598
 DB 306 SDAVPLILGTYNCFMFWASSVSTILNLYHHRNPDTHMSEWIRVFLCWLPIWLRMS 365
 QY 599 RPCRPLILEPTTPCSDTSS---ERKHOILSDVELKERSKSLANVLDIDDDFRHNCRP 655
 DB 366 RPGQ-VGYECPPPPSSSSSSASGKKQOI-ONVELKERSKSLANVLDIDDDFR--CNH 421
 QY 656 MTPCGTLPHPNPAFYRTVYGGDDSGISGPIGST-----RMPDAVTHTCIKSSTYEYELGL 709
 DB 422 RCASATLPHQPTYYRTMYRGDDSGVPGVPGAPVVDGRLHEAIS-HTCLTSSAEYELAL 480
 QY 710 ILKEIRPTDQLRKDDCNDIANDKFAAMVVDRLCIIITFMFAILATIAVLISAPHIIV 769
 DB 481 ILKELRWITELQKKEDTSDITRDWKFAAMVVDRLCIIITFMFAILATIAVLISAPHIIV 540
 QY 770 S 770
 DB 541 S 541
 RESULT 4
 Q9XZ13 ID Q9XZ13 PRELIMINARY; PRT; 496 AA.
 AC Q9XZ13
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DE 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Putative nicotinic acetylcholine receptor alpha 7-1 subunit.
 OS Heliothis virescens (Owlet moth).

RESULT 6

```
Q877S3 PRELIMINARY; PRT; 494 AA.
AC Q87S3;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor Dalphaa subunit variant type I.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalphaa5, Dalphaa6 and Dalphaa7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF321445; AAM13392.1; -
DR FlyBase; FBgn0032151; nacr-alpha-30D.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRfams; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 494 AA; 56095 MW; B46BEDA63A92942 CRC64;

Query Match 40.1%; Score 1622.5; DB 5; Length 494;
Best Local Similarity 61.2%; Pred. No. 2.3e-131;
Matches 319; Conservative 46; Mismatches 77; Indels 79; Gaps 7;

QY 291 SWIFLLIYLNLSAKVCLAGYHEKRLHLLDLPYNTLRLPVNLSDFGLTLMOIID 350
DB 10 SLFVLLIFLAIKESC-QGPEKRLNHLSTYNTLRLPVANSEPLEVFGTLQOIID 68
QY 351 VDEKNOLLTVNWKLEWDMNLWNTSDYGGVKDLRIPHRITWKPDVLMYNSADGFGD 410
DB 69 VDEKNOLLTVNWLNLWDMNDYLNRLWNETYGGVKDLRITPNKWLKPDVLMYNSADGFGD 128
QY 411 TYOTNVVVRNNGSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOLDLQD 470
DB 129 TYHTNVVVRNNGSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOLDLQD 188
QY 471 ETGGDISYVNLGSEWELLGVPGKRNIIYVCCPEYVDITFTIQRIRRTLYFFNLIIPC 530
DB 189 EDGGLDSDFITNGEWLLAMPKKNITVYACCPYVDITFTIQRIRRTLYFFNLIIPC 248
QY 531 VLIASALLGFTLPDPSGKLSIGVTILLSLTVFLNVAETPATSDAVPL----- 581
DB 249 VLISSALLGFTLPDPSGKLSIGVTILLSLTVFLNVAETLPQVSDAIPLLGTYFNCIM 308
QY 582 -----WIRIVFLCWLPLWLRMSRPRPLILEFFPTPC 613
DB 309 FWVASSVLTVVVLYNHHRTADITHMPPIKSVFLQWLPLWLRMSRPRPLILEFFPTPC 359
QY 614 SDTSSERKHOILS-----DVELKERSKSLANVLDIDDDFRNCRNCPWTGGTLPHPNPFY 669
DB 360 -----TRKTLILSNRMKELKERSKSLANVLDIDDDFRHTI----- 398
QY 670 RTVYGGDDSGISGIPGSTRMPDAV-THTTCIKSSTYELGLILKEITFITDOLRKDECN 728
DB 399 -----SGSQTAGSSASFRPTVEEHHTAI-GCNHKDLHLILKELQFITARMRKADDEA 452
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RESULT 7

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Q877S1 PRELIMINARY; PRT; 494 AA.
AC Q87S1;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor Dalphaa subunit variant type
DE III.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalphaa5, Dalphaa6 and Dalphaa7, in Drosophila melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF321447; AAM13394.1; -
DR FlyBase; FBgn0032151; nacr-alpha-30D.
DR InterPro; IPR006201; Neur_chan.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR TIGRfams; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 494 AA; 56113 MW; 48327537229573FF CRC64;

Query Match 40.1%; Score 1620.5; DB 5; Length 494;
Best Local Similarity 61.0%; Pred. No. 3.5e-131;
Matches 318; Conservative 49; Mismatches 75; Indels 79; Gaps 7;

QY 291 SWIFLLIYLNLSAKVCLAGYHEKRLHLLDLPYNTLRLPVNLSDFGLTLMOIID 350
DB 10 SLFVLLIFLAIKESC-QGPEKRLNHLSTYNTLRLPVANSEPLEVFGTLQOIID 68
QY 351 VDEKNOLLTVNWKLEWDMNLWNTSDYGGVKDLRIPHRITWKPDVLMYNSADGFGD 410
DB 69 VDEKNOLLTVNWLNLWDMNDYLNRLWNETYGGVKDLRITPNKWLKPDVLMYNSADGFGD 128
QY 411 TYOTNVVVRNNGSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOLDLQD 470
DB 129 TYHTNVVVRNNGSCLVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFOLDLQD 188
QY 471 ETGGDISYVNLGSEWELLGVPGKRNIIYVCCPEYVDITFTIQRIRRTLYFFNLIIPC 530
DB 189 EDGGLDSDFITNGEWLLAMPKKNITVYACCPYVDITFTIQRIRRTLYFFNLIIPC 248
QY 531 VLIASALLGFTLPDPSGKLSIGVTILLSLTVFLNVAETPATSDAVPL----- 581
DB 249 VLISSALLGFTLPDPSGKLSIGVTILLSLTVFLNVAETLPQVSDAIPLLGTYFNCIM 308
QY 582 -----WIRIVFLCWLPLWLRMSRPRPLILEFFPTPC 613
DB 309 FWVASSVLTVVVLYNHHRTADITHMPPIKSVFLQWLPLWLRMSRPRPLILEFFPTPC 359
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Qy 614 SDTSSERKHQILS-----DVELKERSKSLANLVLDIIDDHRCRPMPTGGTLPHPAFY 669
Db 360 -----TRKILLNSRMKELEKERSKSLANLVLDIIDDHRTI----- 398
Qy 670 RTVYGQDDGSGIGSTRMPDAV-THTTCIKSSTEYELGLILKEIRFITDOLRKDECN 728
Db 399 -----SGSQTAGSSASGFRPTTVEEHHTAI-GCNHKDLHLILKELOFITARMRKADDEA 452
Qy 729 DIANDWFAAMVDRCLLIIFTMFAILATIAVLSAPHIIV 769
Db 453 ELIGDWFAAMVDRFCLVFTLTETIATVTVLSAPHIIV 493

RESULT 8
Q8T7R9
ID Q8T7R9 PRELIMINARY; PRT; 523 AA.
AC Q8T7R9
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Nicotinic acetylcholine receptor Dalpha6 subunit variant type V.
GN NACR-ALPHA-30D OR NACRALPHA-30D OR BCDNA:GH01410 OR CG4128.
OS Drosophila melanogaster (Fruit fly)
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21969411; PubMed=11973307;
RA Grauso M., Reenan R.A., Culetto E., Sattelle D.B.;
RT "Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
RT Dalphas, Dalpha6 and Dalpha7, in Drosophila Melanogaster Identify a
RT New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-
RT Mediated A-to-I Pre-mRNA Editing.";
RL Genetics 160:1519-1533(2002).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF321449; AAMI3396.1;
DR FlyBase; FBgn0032151; nACR-alpha-30D.
DR InterPro; IPR006201; Neur_chan_LBD.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_LBD; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR-ION_CHANNEL; 1.
DR Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 523 AA; 59110 MW; 1C200AF74F87F841 CRC64;

Query Match 39.8%; Score 1611; DB 5; Length 523;
Best Local Similarity 58.2%; Pred. No. 2.5e-130;
Matches 320; Conservative 46; Mismatches 76; Indels 108; Gaps 7;

Qy 291 SWIFLLIYNLSAKVCLAGYHEKRLHLLDLPYNTLPRVNLNEDSPQLSFGLTLMQIID 350
Db 10 SLFVLLIPLAIKESQ-QGPEKRLNLLHLLTYNTLPRVANESPELVKFGTLQIID 68

Qy 351 VDEKNQLLVTVNLKLENDMLRWNTSDYGGVKDLRIPPHRIKPKDVLVYNSADEGFDG 410
Db 69 VDEKNQLLVTVNLKLENDMLRWNTSDYGGVKDLRIPPHRIKPKDVLVYNSADEGFDG 128

Qy 411 TYQTNVVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGFQDLQIQD 470
Db 129 TYHNVVVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGNQDLVYNS 188

Qy 471 ETGGDISYVLNGEWELGVPGKRIEYNYCCPEYIDITFAIIRRTLYFFNLIIPC 530
Db 189 EDGGLSDFITNGEWYLLAMPKKNITVIYACPEPYVDITFTIQRRTLYFFNLIIPC 248

Qy 531 VLIASMLLGLTLPDSDGKILSGVTILLSITVFLNVAESMPTTSDAVPLIGVITLLSL 581
Db 126 NVVVRSGSLYVPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGNQDLVYNSADEG 185
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Db 249 VLISSMLLGLTLPDSDGKILSGVTILLSITVFLNVAESMPTTSDAVPLIGVITLLSL 308
Qy 582 -----WIR 584
Db 309 TVFLNLVAETLPQVSDAIPLLGTGYFNCIMFMVASSVVLTVVVLNHHRTADHEMPWIK 368
Qy 585 IVFLCWLPWILMSRPGRLILEPTTPCSDTSSERKHQILS-----DVELKERSKSLA 640
Db 369 SVFLQWLPWILRMGRGRKI-----TRKILLNSRMKELEKERSKSLA 414
Qy 641 NVLDIDDDHRCRPMPTGGTLPHPAFYRTVYGGDDSGIGSTRMPDAV-THTTCI 699
Db 415 NVLDIDDDHRTI-----SGSQTAGSSASGFRPTTVEEHHTAI 453
Qy 700 KSSTEYELGLILKEIRFITDOLRKDECNDIANDWFAAMVDRCLLIIFTMFAILATIA 759
Db 454 -GCNKHDLHLILKELQFITARMRKADDEAELIGDWFAAMVDRFCLVFTLTETIATV 512
Qy 760 VLSAPHIIV 769
Db 513 VLSAPHIIV 522

RESULT 9
Q9XZ14
ID Q9XZ14 PRELIMINARY; PRT; 501 AA.
AC Q9XZ14;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Putative nicotinic acetylcholine receptor alpha 7-2 subunit.
OS Heliothis virescens (Noctuid moth) (Owlet moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea;
OC Noctuidae; Heliothinae; Heliothis.
OX NCBI_TaxID=7102;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte T., Oellers N., Adamczewski M.;
RT "Putative alpha subunits of insect nicotinic acetylcholine receptors
RT more similar to vertebrate alpha 7 subunits and C. elegans Ce21 than
RT to other insect nicotinic acetylcholine receptor alpha subunits.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
DR EMBL; AF143847; AAD32698.1;
DR InterPro; IPR006201; Neur_chan_LBD.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006029; Neur_chan_LBD.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_LBD; 1.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR-ION_CHANNEL; 1.
DR Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;
KW Transmembrane.
SQ SEQUENCE 501 AA; 56704 MW; 43CB0DC3960C78AB CRC64;

Query Match 39.8%; Score 1609; DB 5; Length 501;
Best Local Similarity 60.8%; Pred. No. 3.5e-130;
Matches 319; Conservative 57; Mismatches 65; Indels 84; Gaps 10;

Qy 295 LLIYLNLSAKVCLAGYHEKRLHLLDLPYNTLPRVNLNEDSPQLSFGLTLMQIIDVDEK 354
Db 10 LLLLPVSEQ-----GPHEKRLNLLHLLTYNTLPRVANESPELVKFGTLQIIDVDEK 65

Qy 355 NQLLVTVNLKLENDMLRWNTSDYGGVKDLRIPPHRIKPKDVLVYNSADEGDTYQT 414
Db 66 NQLLVTVNLKLENDMLRWNTSDYGGVKDLRIPPHRIKPKDVLVYNSADEGDTYQT 125

Qy 415 NVVVRNNGSLYVPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGFQDLQIQDDETG 474
Db 126 NVVVRSGSLYVPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGNQDLVYNSADEG 185
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Db 129 TYHTNIVKHNSCLYVPPGIFKSTCKIDITWFPDDQHCCKMFGSWTYDGNQLDLVLS 188
QY 471 ETGGDISSVLVNGEWELGV-PGK-----RNEYYNCCPEPYDITFAIII 515
Db 189 EGGDLSDFITNGEWLVGHAGKEEYDSLRLPRTICRYHLYYT-NSSPYI----- 239
QY 516 RRTLYFFPNLIIPCVLIASM-----ALLGFTLPDPSGE----- 549
Db 240 ----ILFFQFN-----CAMCANLIDGPTGLHIAAGFGRDAGRTDAGNYITIINSISKPCRRVHA 292
QY 550 ----KLSLG-----VTLLSLTVFLNKNVETMPA 574
Db 293 DNVGCCSSRYTHITLKRYSLKYPGRTIDHYOCRAERVITLLSLTVFLNVAETLPQ 352
QY 575 TSDAVPL-----WIRIVFLCWLPLWLRM 597
Db 353 VSDAIPLLGTYFCINFMWVASSVLTVVVLVNYHRTADIHMPWIKSVFLQWLFWLRM 412
QY 598 SRGPRPLILEPPTPCSDTSSERKHOILS-----DVELKERSKSLANVLDDDFRHC 653
Db 413 GRPGRKI-----TRKTILLSNRKMLEKERSKSLANVLDDDFRHTI 458
QY 654 RPTWPGTLPHPAFYRTVYGDDGSGIGTIGTIDYOCRAERVITLLSLTVFLNVAETLPQ 712
Db 459 -----SGSQTAGSSASFGRTPTVEBHHTAI-GCNHKLHLILK 496
QY 713 EIRFITDQLRKDDCNDIANDKFAVMYVDRLCLIFTFMFAILATIAVLVLSAPHIV 769
Db 497 ELQFITARKKADDEALIGDKMFAVMYVDRLCLIFTFMFAILATIAVLVLSAPHIV 553

RESULT 13
Q8IPE2
ID Q8IPE2 PRELIMINARY; PRT; 525 AA.
AC Q8IPE2
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CG4128-PC.
GN NACRALPHA-30D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA April J.F., Adayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballwe R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busan M.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Dou L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M.E., Kalish B., Karp G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson J.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacble J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reibert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celnik S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Ananides P.G., Brandon R.C., Rogers Y.,
RA Banson J., An H., Baldwin D., Banson J., Beeson K.Y., Busan D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacble J., Paragas V., Park S., Patel S., Pfeiffer B.,
RA Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Bereman B., Carlson J.W., Celnik S.E.,
RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celnik S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA Flybase:
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003626; AAN10709.1;
SQ SEQUENCE 525 AA; 60135 MW; CF95283C56EA90A9 CRC64;

Query Match 30.5%; Score 1235; DB 5; Length 525;
Best Local Similarity 47.5%; Pred. No. 7.4e-98;
Matches 270; Conservative 53; Mismatches 103; Indels 142; Gaps 15;

QY 291 SWIFLLIYLNLSAKVCLAGYHEKRLHLLDLPYNTLRLPVLNESPQLQSLFGLTLMQIID 350
Db 10 SLFVLLIFLAIKESC-OGPHEKRLNHLSTYNTLRLPVLNESPQLQSLFGLTLMQIID 68
QY 351 VDEKNQLLVNVLKLEWNNMLRWNTSDYGGVKDLRIPPHRIKWPDLVLYNSADEGFDG 410
Db 69 VDEKNQLLVNVLKLEWNNMLRWNTSDYGGVKDLRIPPHRIKWPDLVLYNSADEGFDG 128
QY 411 TYOTNVVNRNGSCLYVPPGIFKSTCKIDITWFPDDQHCCKMFGSWTYDGNQLDLVLS 470
Db 129 TYHTNIVKHNSCLYVPPGIFKSTCKIDITWFPDDQHCCKMFGSWTYDGNQLDLVLS 188
QY 471 ETGGDISSVLVNGEWELGV-PGK-----RNEYYNCCPEPYDITFAIII 515
Db 189 EGGDLSDFITNGEWLVGHAGKEEYDSLRLPRTICRYHLYYT-NSSPYI----- 239

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OY 516 RRTLYEYFNLIIPCVLIASM-----ALLGFTLPDPDSCEKLS----- 552
Db 240 ---ILFFQFN---CAMCANLIDGFTGLHIAAGREGTADAGRNTYTIINSISKPCRRVHA 292
OY 553 -----LGVTI-----LGLSLTVFLNMVA 569
Db 293 DNVGCCSYRTHYTHILKRYSLKYGPIGTIDHYHYYQCRAEITYFNCIMFWASSVVLTVVV 352
OY 570 ---ETMPATSDAVPLWIRIVFLCWLPLWLRMRSPRGLPILLEFPPTPCSDTSSERKHQTLIS 626
Db 353 LNYHRTADIHEMPWPWIKSVFLWLPWLRLMRGPRKI-----TRKTILLS 398
OY 627 ----DVELKERSKSLANVIDIDDDFRHNCPRMTPGGTLPHNPAFYTVYVGGDDGSIG 682
Db 399 NRMKELELKERSKSLANVIDIDDDFRHTI-----SGSQTAIG 437
OY 683 PIGSTRMPDAY-THHTCKISSTVEYELGLILKEIRFITDOLRDKDCNDIANDWKFAMV 741
Db 438 SSASFGRPRTVEEHHTAI-GCNKDLHLILKELOFITARMKRKADDEALIGDWKFAAMV 496
OY 742 DRLCLLIPTFAILATVALLSAPHIIV 769
Db 497 DRFCILVETLTIIATVTLISAPHIIV 524

RESULT 14
O9VJT9 PRELIMINARY; PRT; 273 AA.
AC O9VJT9
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-OCT-2002 (TremBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)
DE CG4498 protein.
GN NACR-ALPHA-34E OR NACRALPHA-34E OR BG:DS05899.4 OR BG:DS05899.5 OR
OS CG4498 OR CG16878.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.:
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
RA Ibegwam C., Jalali M., Kruse D., Li P., Mattel B., Moshrefi A.,
RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
RA Pacleb J., Paragov V., Park S., Patel S., Pfeiffer B.,
RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
RT "Sequencing of Drosophila melanogaster genome."
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
RT "Annotation of Drosophila melanogaster genome."
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA FlyBase;
RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AE003642; AAF53374.2;
DR HSP; P58154; 119B.
DR FlyBase; FBgn028875; nACR-alpha-34E.
DR InterPro; IPR008201; Neur_channel.
DR InterPro; IPR006202; Neur_channel_LBD.
DR InterPro; IPR006029; Neur_channel_memb.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
SQ SEQUENCE 273 AA; 31655 MW; CA95F19953E37248 CRC64;
Query Match 29.3%; Score 1186; DB 5; Length 273;
Best Local Similarity 57.2%; Pred. No. 5e-94;
Matches 243; Conservative 13; Mismatches 17; Indels 152; Gaps 7;
Oy 346 MQITDVEKNOLLVTNVWLKLEWMDMLRWNTSYGGVKDLRIPIPHRTWKPDVLMYNSAD 405
Db 1 MQITDVEKNOLLVTNVWLKLEWMDMLRWNTSYGGVKDLRIPIPHRTWKPDVLMYNSAD 60
Oy 406 EGFDTGTQTNVVRNNGSCLVPPGIFKSTCKIDITWPFDDQRCMKFGSWTYDGFOLD 465
Db 61 EGFDTGTQTNVVRNNGSCLVPPGIFKSTCKIDITWPFDDQRCMKFGSWTYDGFV - 119
Oy 466 LQLQDETGGDISSYVLNGEWELLGVPGKRNIYYNCCPEPIDITFAIIIRRTLYEYFN 525
Db 120 -----W-FSVPGKRNIYYNCCPEPIDITFAIIIRRTLYEYFN 158

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Qy	526	LIIPCVLIASALLGFTLPDPSGEKLSGLGVTILLSLVFLNVAETMPATSDAVPLMIRI	585
Db	159	LIIPCVLIASALLGFTLPDPSGEKLSGLGVTILLSLVFLNVAETMPATSDAVPLMIRI	205
Qy	586	VFLCWLPLILRMSRPGRLILEPTTPCSDTSSEKHKQILSDVELKERSKSLANVLDI	645
Db	206	VFLCWLPLILRMSRPGRLILEPTTPCSDTSSEKHKQILSDVELKERSKSLANVLDI	210
Qy	646	DDDFRHNCRPMTFEGTLPHPNPAFYRTVYGGDDGSGIGSTRMPDAVTHHTCIKSSTEY	705
Db	211	DDDFRHNCRPMTFEGTLPHPNPAFYRTVYGGDDGSGIGSTRMPDAVTHHTCIKSSTEY	218
Qy	706	ELGLILKEIRFTDQLRKDECDNDIANDWKFAMVVDRLCLIFTMFAIATIAVLISAP	765
Db	219	ELGLILKEIRFTDQLRKDECDNDIANDWKFAMVVDRLCLIFTMFAIATIAVLISAP	268
Qy	766	HIIVS 770	
Db	269	HIIVS 273	
RESULT 15			
ID	Q9JHD6	PRELIMINARY; PRT; 502 AA.	
AC	Q9JHD6		
DT	01-OCT-2000	(TrEMBLrel. 15, Created)	
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)	
DT	01-MAR-2003	(TrEMBLrel. 23, Last annotation update)	
DE	Nicotinic acetylcholine receptor subunit alpha 7.		
GN	CHRNA7.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=DBA/2Ibg;		
RX	MEDLINE=97189245; PubMed=9037516;		
RA	Stitzel J.A., Farnham D.A., Collins A.C.;		
RT	"Linkage of strain-specific nicotinic receptor alpha 7 subunit		
RT	restriction fragment length polymorphisms with levels of alpha-		
RT	bungarotoxin binding in brain."		
RL	Brain Res. Mol. Brain Res. 43:30-40(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=DBA/2Ibg;		
RA	Stitzel J.A.;		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.		
DR	EMBL; AF225980; AAF35885.1;		
DR	MGI; 99779; Chrna7.		
DR	InterPro; IPR006201; Neur_Channel.		
DR	InterPro; IPR008202; Neur_Channel_LBD.		
DR	Pfam; PF02931; Neur_chan_memb.		
DR	Pfam; PF02932; Neur_chan_LBD; 1.		
DR	PRINTS; PR00252; NRIONCHANNEL.		
DR	TIGRFAMs; TIGR00860; LIC; 1.		
DR	PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.		
KW	Glycoprotein; Ionic channel; Postsynaptic membrane; Receptor;		
KW	Transmembrane.		
SK	SEQUENCE 502 AA; 56617 MW; C9353E5136D620E3 CRC64;		
Query Match			
Best Local Similarity 29.38; Score 1185.5; DB 11; Length 502;			
Matches 243; Conservative 79; Mismatches 115; Indels 85; Gaps 12;			
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Db	8	IWLALAAALLHVSLOGEFQRLYKELVKNPLRPNVANDSOPLTVYVFSLSLIQIMDVE	67
Qy	354	KNQLLVTVNWLKLEWDMNLRWNTSDYGGVKDLRIPPHRIWKPDVLMYNSADEGFDGTYQ	413

Db	68	KNQVLTNTNWLQMSWTQDHYLQNNMSEYPGVKNVRFDPGQIWKPDILLYNSADERDATFH	127
Qy	414	TNVVVRNNGSLVYPPGIFKSTCKIDITWFPDDQRCMEKFGSWTYDGFOLDLQDBTG	473
Db	128	TNVLVNASGHCOYLPPOGIFKSCYIDVRWFPDFVOQCKLFGSGWSYGLDLOMQE---	184
Qy	474	GDISSYVLNGEWELLVGPGKRNEYNNCCPEPYIDITFAIIRRTLYYFNLIIPCVLI	533
Db	185	ADISSYIPNGEWDLMGIPGKRNEKFEYCKPEYPDVTYVTVMRRRTLYYGLNLLIPCVLI	244
Qy	534	ASMAILGFTLPDPSGEKLSGLGVTILLSLVFLNVAETMPATSDAVPL	581
Db	245	SALALLVFLLPADSGEKISLGITVLLSUTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV	304
Qy	582	-----WIRIVFLCWLPLILRMSRPG-----RPLILEFFPTP	612
Db	305	GLSVVTVTVIVLYHHHDPDGGKMPKWTRIIILNWCANFLMKRFGEDKVRPACQHKPRR-	363
Qy	613	CSDTSSEKHKQILSDVELKERS--KSLANVLDIDDDFR-----HNCRMPGPGTLPHPNPA	667
Db	364	CS-----LASVELSAGAGPPSSNGNLLYI--GFRGLEGMHCAP--TP-----	401
Qy	668	FYRTVYGGDDGSI-GPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFTDQLRKDDE	726
Db	402	-----DSGVVCGRLACSPTHDEHLMHGTHPSDGDGPDILAKILEEVRYIANRFRCODE	452
Qy	727	CNDIANDWKFAMVVDRLCLIFTMFAIATIAVLISAPHII 768	
Db	453	SEVICSEWKKFAACVVDRLCLMAFSVFTIICIGILMSAPNEV 494	

Search completed: August 13, 2003, 15:29:07
Job time : 76.6446 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:55 ; Search time 16.1234 Seconds
(without alignments)
2245.843 Million cell updates/sec

Title: US-09-303-232-2
Perfect score: 4043
Sequence: 1 MRNAQLKTEVDDELWLAV.....MFAILATIAVLLSAPHIIVS 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1182.5	29.2	502	1	ACH7_MOUSE
2	1179.5	29.2	502	1	ACH7_CHICK
3	1173.5	29.0	502	1	ACH7_RAT
4	1159.5	28.7	502	1	ACH7_HUMAN
5	1157	28.6	499	1	ACH7_BOVIN
6	1104	27.3	498	1	ACH1_CAEEL
7	888	22.0	567	1	ACH1_DROME
8	886	21.9	516	1	ACH1_MANSE
9	873	21.6	557	1	ACH1_SCHGR
10	848.5	21.0	529	1	ACH2_HUMAN
11	845	20.9	503	1	ACH3_HUMAN
12	843.5	20.9	576	1	ACH2_DROME
13	840	20.8	521	1	ACH3_DROME
14	838	20.7	528	1	ACH2_CHICK
15	827.5	20.5	456	1	ACHA_CHICK
16	827.5	20.5	496	1	ACH3_CHICK
17	827	20.5	511	1	ACH2_RAT
18	823	20.4	499	1	ACH3_RAT
19	820.5	20.3	495	1	ACH3_BOVIN
20	820.5	20.3	512	1	ACH3_CARAU
21	815.5	20.2	519	1	ACH4_DROME
22	805	19.9	498	1	ACH6_DROME
23	803	19.9	494	1	ACH6_HUMAN
24	801	19.8	457	1	ACHA_BOVIN
25	799	19.8	494	1	ACH6_HUMAN
26	797	19.7	457	1	ACHA_MOUSE
27	794.5	19.7	457	1	ACH2_XENLA
28	792.5	19.6	493	1	ACH6_RAT
29	791.5	19.6	538	1	ACH8_CAEEL
30	789	19.5	457	1	ACHA_RAT
31	789	19.5	470	1	ACHP_CHICK
32	787	19.5	491	1	ACHN_CHICK
33	786.5	19.5	456	1	ACHA_BRARE

34	785	19.4	461	1	ACHA_TORMA	P02711	torpedo mar
35	783	19.4	495	1	ACHP_RAT	P12392	rattus norv
36	782.5	19.4	500	1	ACHN_RAT	P12390	rattus norv
37	782	19.3	502	1	ACHN_HUMAN	P17787	homo sapien
38	780	19.3	482	1	ACHA_HUMAN	P02708	homo sapien
39	780	19.3	627	1	ACHA_HUMAN	P43681	homo sapien
40	779.5	19.3	622	1	ACHA_CHICK	P09482	gallus gall
41	779.5	19.3	461	1	ACHA_TORCA	P02710	torpedo cal
42	773.5	19.1	457	1	ACH1_XENLA	P22456	xenopus lae
43	772	19.1	464	1	ACHO_RAT	P12391	rattus norv
44	769.5	19.0	459	1	ACHN_CARAU	P19370	carassius a
45	768	19.0	630	1	ACH4_RAT	P09483	rattus norv

ALIGNMENTS

RESULT 1
ACH7_MOUSE
ID ACH7_MOUSE STANDARD; PRT; 502 AA.
AC P49582;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR ACRA7
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=Brain;
RX MEDLINE=95324936; PubMed=7601470;
RA Orr-Urtreger A., Seldin M.F., Baldini A., Beaudet A.L.;
RT "Cloning and mapping of the mouse alpha 7-neuronal nicotinic
acetylcholine receptor.";
RL Genomics 26:399-402(1995).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
MEMBRANE.
CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

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or send an email to license@isb-sib.ch).

EMBL; L37663; AAC42053.1; -
PIR; A57175; A57175.
MGD; MGI:95779; Chnra7.
InterPro; IPR006029; Neu_channel_memb.
InterPro; IPR006202; Neur_chan_IAB.
DR InterPro; IPR006201; Neur_channel.
DR Pfam; PF02931; Neur_chan_IAB; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PRO0252; NRIONCHANNEL.
DR TIGRFAMs; TIGR00860; LIC; 1.
DR P04756 mus musculus
P05377 xenopus lae
P43143 rattus norv
P45963 caenorhabdi
P25108 rattus norv
P26153 gallus gall
P09484 rattus norv
Q98880 brachydanio

FT CHAIN 1 22 BY SIMILARITY.
FT CHAIN 23 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT DOMAIN 23 230 ALPHA-7 CHAIN.
FT EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 231 255 POTENTIAL.
FT TRANSMEM 262 280 POTENTIAL.
FT TRANSMEM 296 317 POTENTIAL.
FT DOMAIN 318 469 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 470 490 POTENTIAL.
FT DISULFID 150 164 BY SIMILARITY.
FT DISULFID 212 213 ASSOCIATED WITH RECEPTOR ACTIVATION
FT (BY SIMILARITY).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 502 AA; 56631 MW; C9312E5226D120E3 CRC64;

Query Match 29.2%; Score 1182.5; DB 1; Length 502;
Best Local Similarity 45.8%; Pred. No. 2.8e-75;
Matches 239; Conservative 80; Mismatches 118; Indels 85; Gaps 10;

QY 297 IYLNLSA---KVLGAGYHEKRLHLLDLPYNTLPRVNLNESDPLQSLFGLIMLIQIDVDE 353
DB 8 IWLALAAALLHVSQGEFQRLYKELVKNYNPLERPVANDSQPLVYFSLQLQIMDYDE 67
QY 354 KNOILVTNWLKLENNMNLNRNTSDYGVKDLRTPPHRIKPKDVLNYSADGEGDTYQ 413
DB 68 KNOVLITNWLQMSWDHYLQNMSEYPCVKNVRFPDQGIWKPDILLYNSADEREDATFH 127
QY 414 TNVVVNRNSCLYVPPGIFKSTCKIDITWFFPDQRCCEMKGSTWYDGFQDLQLODETG 473
DB 128 TNVLNASHCQYLPPIGIFKSCYIDVRWFPDVOQCKLKFGSWSYGCWSLDLQMQE--- 184
QY 474 GDISSVYLVNGEWELGVGCKRNEIYVNCPEYIDITFAIIRRTLYFFNLIIPCVLI 533
DB 185 ADISSYIFNGEWMGIFGKREKEFYECPEYDVTYVTRRRRTLYGLNLLIPCVLI 244
QY 534 ASMALIGFTLPDSEKISLGVITLLSLTVFLNVAETPATSDAVPL----- 581
DB 245 SALALVFLLPADSEKISLGVITLLSLTVFLNVAETPATSDSVPLIAQYFASTMIV 304
QY 582 -----WIRIVLCWLPWILMRSPG-----RPLILEFPPTP 612
DB 305 GLSVVTVTVILRYHHDPDGGKMPKWTIRILLNCAWFLMKRPGEDKVRPACQHKPR- 363
QY 613 CSDTSSERKHOILSDVELKRSKSLANVLIDDDERHCRPMPGGLPHNPAFYRT 672
DB 364 CS-----LASVELSAGAG-----PPTSNGNLV--IGFRGL 392
QY 673 YGQ-----GDGSI-GPIGSTRMPDAVTHHTCIKSTSEYELGLILKEIRFTDQLRKDE 726
DB 393 EGMHCAPTDSGVVCGRLACSPHDEHLMHGTHPSDGDPLAKILEEVRYIANRRCQDE 452
QY 727 CNDIANDKFRAMVVDRLCLLIFTMFPAIATIAVLLSAPHII 768
DB 453 SEVICSEKFAACVVDRLCLMAFSVFTIICIGILMSAPNFV 494

RESULT 2
ACH7_CHICK
ID ACH7_CHICK STANDARD; PRT; 502 AA.
AC P22770;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=91097796; PubMed=1702646;
RA Couturier S., Bertrand D., Matter J.M., Hernandez M.C., Bertrand S.,
RA Millar N., Valera S., Barks T., Ballivet M.;

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RT "A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is
RT developmentally regulated and forms a homo-oligomeric channel blocked
RT by alpha-BTX."
RL Neuron 5:847-856(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90315158; PubMed=2369519;
RA Schoeffer R., Conroy W.G., Whiting P., Gore M., Lindstrom J.;
RA "Brain alpha-bungarotoxin binding protein cDNAs and MABs reveal
RT subtypes of this branch of the ligand-gated ion channel gene
RT superfamily."
RL Neuron 5:35-48(1990).
RN [3]
RP SEQUENCE OF 1-18 FROM N.A.
RC STRAIN=White leghorn; TISSUE=Erythrocyte;
RX MEDLINE=93049204; PubMed=1425587;
RA Matter-Sadzinski L., Hernandez M.C., Rostocil T., Ballivet M.,
RA Matter J.M.;
RT "Neuronal specificity of the alpha 7 nicotinic acetylcholine receptor
RT promoter develops during morphogenesis of the central nervous
RT system."
RL EMBO J. 11:4529-4538(1992).
RN [4]
RP SEQUENCE OF 24-47.
RC TISSUE=Brain;
RX MEDLINE=85270494; PubMed=3860855;
RA Conti-Troconci B.M., Dunn S.M.J., Barnard E.A., Dolly J.O., Lai F.A.,
RA Ray N., Raftery M.A.;
RT "Brain and muscle nicotinic acetylcholine receptors are different but
RT homologous proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 82:5208-5212(1985).
RN [5]
RP MUTAGENESIS OF LEU-270.
RX MEDLINE=92049732; PubMed=1719423;
RA Recaf F., Bertrand D., Galzi J.-L., Devillers-Thiery A., Mulle C.,
RA Hussy N., Bertrand S., Ballivet M., Changeux J.-P.;
RT "Mutations in the channel domain alter desensitization of a neuronal
RT nicotinic receptor."
RL Nature 353:846-849(1991).
RN [6]
RP MUTAGENESIS TO CONVERT ION SELECTIVITY FROM CATIONIC TO ANIONIC.
RX MEDLINE=93024917; PubMed=1383829;
RA Galzi J.-L., Devillers-Thiery A., Hussy N., Bertrand S.,
RA Changeux J.-P., Bertrand D.;
RT "Mutations in the channel domain of a neuronal nicotinic receptor
RT convert ion selectivity from cationic to anionic."
RL Nature 359:500-505(1992).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- DEVELOPMENTAL STAGE: ALPHA-7 TRANSCRIPTS TRANSIENTLY ACCUMULATE
CC IN THE DEVELOPING OPTIC TECTUM BETWEEN E5 AND E16.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
DB EMBL; X52295; CAA36543.1; -
DR EMBL; X68246; CAA48317.1; -
DR EMBL; X68586; CAA48576.1; -
DR PIR; JN0113; JN0113.
DR PDB; 1KC4; 17-APR-02.

```

DR PDB: 1KL8; 17-APR-02.
DR InterPro: IPR006029; Neu_channel_memb.
DR InterPro: IPR006202; Neur_chan_LBD.
DR InterPro: IPR006201; Neur_channel.
DR Pfam: PF02931; Neur_chan_LBD; 1.
DR Pfam: PF02932; Neur_chan_memb; 1.
DR PRINTS: PR00252; NRIONCHANNEL.
DR TIGRFAMS: TIGR00860; LIC; 1.
DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family; 3D-structure.
FT SIGNAL 1 23
FT CHAIN 24 502 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT ALPHA-7 CHAIN.
FT EXTRACELLULAR.
FT DOMAIN 24 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT DOMAIN 318 469
FT TRANSMEM 470 490
FT DISULFID 150 164
FT DISULFID 212 213
FT ASSOCIATED WITH RECEPTOR ACTIVATION
FT (BY SIMILARITY).
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT MUTAGEN 270 270 L->S,T: SUPPRESSES INHIBITION BY THE
FT OPEN-CHANNEL BLOCKER QX-222.
FT OR -> ET (IN REF. 3).
FT CONFLICT 26 27
FT SEQUENCE 502 AA; 56946 MW; 572325D4309AD2FD CRC64;
Query Match 29.2%; Score 1179.5; DB 1; Length 502;
Best Local Similarity 45.7%; Pred. No. 4.6e-75;
Matches 237; Conservative 80; Mismatches 127; Indels 75; Gaps 9;
QY 295 LLIYLNLSA--KVLGAGYHEKLLDLDLPNTLPRVNLSDPLQLSFLGLTLMQIIDV 351
DB 6 LMLWLLAAGLVRESLQGEFORLYKELLNKLNPLRPVANDSQPLTVYFTLSLMQIMDV 65
QY 352 DEKNQLLVNTVMKLEWNDMNLRWNTSDYGGYKDLRIPPHRTKPDVLMVNSADEGFCGT 411
DB 66 DEKNQVLTTNIWLMYWTBHYLQWNVSEYGVKNVRFDPGLWKPDILLYNSADERFAT 125
QY 412 YQTNVVRNNGSLYVPGGIFKSTKIDITWPFDDQRCMKFGSWTYDGFOLDLQDE 471
DB 126 FHTNVLVNSGHCQYLPPLGPIFKSSCYIDVRPFQKCNLKGWSWTYGGWSLDLQMQE- 184
QY 472 TGGDISSYVLNGEWELLGVGKRNELYYNCCPEYIDITFAIIRRTLYYFNLIPCV 531
DB 185 --ADISGYISNGEWDLVGIPGKRTSEFYECCKEYDPDITFTVMRRRTLYYGLNLLIPC 242
QY 532 LIASMLLGLFTLPDPSGKLSLGVTLISLITVFLNVAETMPATSDAVPL----- 581
DB 243 LISALALLVFLPADSGEKISLGITVLLSLITVFMLLVAEIMPATSDVFLIAQYFASTMI 302
QY 582 -----WTRVFLCWLPMILMRSPGRPLILEFFTPPCS 614
DB 303 IVGLSVVVTVIVLQYHHHPDGGKMPKTRVILLANCAWFLMRKRP-----EDKVRPAC 357
QY 615 DTSSERKHQILSDVELKERSSKLL-ANVLDIDDDPRH---NCRPMTGGTLPHPNAPY 669
DB 358 QHKQRCS--LSSMENVTVSGQCSGNMLYI--GFRGLDGVHCTPTTDSGVI----- 406
QY 670 RTVYGGDGSIGPIGSTRMPAVTHHTCIKSTYELGLILKEIRFIQDLQRKDCMD 729
DB 407 -----CGRWTCSTEEENLHSGHPSEGGPDIAKILEEYVIANRFDQDEEA 455
QY 730 IANDWKFAAMVDRLCLITFTFAIATIAVLLSAPHII 768
DB 456 ICNEMKFAASVVDRLCLMAFSVETICTIGILMSAPNFV 494

RESULT 3

ACH7_RAT
ID ACH7_RAT STANDARD; PRT; 502 AA.
AC Q05941;
DT 01-FEB-1994 (rel. 28, Created)
DT 01-FEB-1994 (rel. 28, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR ACRA7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1] SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=93147931; PubMed=7678857;
RA Seguela P., Wadiche J., Dineley-Miller K., Dani J.A., Patrick J.W.;
RT "Molecular cloning, functional properties, and distribution of rat
brain alpha 7: a nicotinic cation channel highly permeable to
calcium.";
RT J. Neurosci. 13:596-604(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Boulter J.;
RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISION TO 363.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RA Hartley M.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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CC -----
DR EMBL; S53987; AAC25224.2; -;
DR EMBL; L31619; AAC33136.1; -;
DR PIR; T01378; T01378.
DR InterPro: IPR006029; Neu_channel_memb.
DR InterPro: IPR006202; Neur_chan_LBD.
DR InterPro: IPR006201; Neur_channel.
DR Pfam: PF02931; Neur_chan_LBD; 1.
DR Pfam: PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 22
FT CHAIN 23 502 BY SIMILARITY.
FT NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
FT ALPHA-7 CHAIN.
FT DOMAIN 23 230
FT TRANSMEM 231 255
FT TRANSMEM 262 280
FT TRANSMEM 296 317
FT DOMAIN 318 469
FT TRANSMEM 470 490
FT DISULFID 150 164
FT DISULFID 212 213
FT BY SIMILARITY.
FT ASSOCIATED WITH RECEPTOR ACTIVATION

```
FT CARBOHYD 46 46 (BY SIMILARITY).
FT CARBOHYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 447 447 N -> F (IN REF. 2).
FT CONFLICT 469 469 P -> R (IN REF. 2).
SQ SEQUENCE 502 AA: 56410 MW: 00996674EC7B9A56 CRC64;

Query Match 29.0%; Score 1173.5; DB 1; Length 502;
Best Local Similarity 45.6%; Pred. No. 1.2e-74;
Matches 238; Conservative 80; Mismatches 119; Indels 85; Gaps 10;

QY 297 IYLNLSA---KVLGAGHYEKLLHDLDPYNTLPRPVNSDPLQSLFGLTQIMQIDVDE 353
DB 8 IWLALAAHLSVQLQGEQRRLYKELVKNYPLRPVANDSQPLTVYFSLSLQIMQIDVDE 67

QY 354 KNOLLTVNVLKLEWMDNLRWNTSDYGGVKKDLRIIPHRWKPDVLMVNSADEGFDGTYQ 413
DB 68 KNQVLTNIWQLQSWTDHYLQWNSYPGVKNRFPDQGIWKPDILLNSADERFATFH 127

QY 414 TNYVVRNNGSLYPPPGIFKSTCKIDITWFFPDQRCMKFGSWTYDGFQDLQQLDQDTG 473
DB 128 TNLVNASGHCOYLPPGIFKSTCKIDITWFFPDQRCMKFGSWTYDGFQDLQQLDQDTG 473

QY 474 GDSSVYLVNGEWELLGVPGKNEIYNYCCPEYDITFAIIRRTLYFFNLIPCVLI 533
DB 185 ADISYIPNGEWMGLMGPGRKNEFYECCKPEYDVTYVTVMTTRRTLYYGLNLIPCVLI 244

QY 534 ASMALGFTLPDQSGEKLGLVTLISLTVLNVAETMPATSDAVPL----- 581
DB 245 SALALLVFLPADSGEKISLIGTVLLSLTVFLLVAEIMPATSDVPLIAQYFASTMIIV 304

QY 582 -----WIRIVFLCWLPWLRLMSRPG-----RPLILEFFPTP 612
DB 305 GLSVVTVTVILRYHHDPDGGKMPKWKTRILLNWCAMFLMRKPGEDKVRPACQHKPRR- 363

QY 613 CSDFSSEKHOILSDVELKRSKSLANVLDDDDPHNCRPMTPGTLPHNFAFYETV 672
DB 364 CS-----LASVELSAGAG-----PPTSGNGLLY--IGFRL 392

QY 673 YGQ-----GDGSI-GPTGSRMPDAVTHHTCIKSTSEYELGLILKEIRFTDQLRKDE 726
DB 393 EGMHCAPTDSGVVCGRLACSPTHDEHLMHGHPDGDPLAKILEEVRYIANRRCODE 452

QY 727 CNDIANDWKFAAMVDRCLIFTFMFAIATIAVLLSAPHII 768
DB 453 SEVICSEWKAACVVDPLCLMAFSVFTICTIGILMSAPNEV 494

RESULT 4
ACH7_HUMAN STANDARD; PRT: 502 AA.
AC P36544; Q15826; Q96RH2; Q99555; Q9BXH0;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.
GN CHRNA7 OR NACHRA7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=94195283; PubMed=8145738;
RA Peng X., Katz M., Gerzanich V., Anand R., Lindstrom J.;
RT "Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit
RT from the SH-SY5Y cell line and determination of pharmacological
RT properties of native receptors and functional alpha 7 homomers
RT expressed in Xenopus oocytes.";
RL Mol. Pharmacol. 45:546-554(1994).
RN [2]

SEQUENCE FROM N.A.
TISSUE=Hippocampus;
RA Logel J., Drobning C., Barnhart M., Antle C., Leonard S.;
RN Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
MEDLINE=97062879; PubMed=8906617;
RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
RT beta 4 subunits.";
RL J. Mol. Neurosci. 7:217-228(1996).
[4]
SEQUENCE FROM N.A.
MEDLINE=97162233; PubMed=9009220;
RA Groot Kormelink P.J., Luyten W.H.M.L.;
RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
RT nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
RT expression of seven nAChR subunits in the human neuroblastoma cell
RT line SH-SY5Y and/or IMR-32.";
RL FEBS Lett. 400:309-314(1997).
[5]
REVISONS.
RP Groot Kormelink P.J., Luyten W.H.M.L.;
RA Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
TISSUE=Epidermal keratinocytes;
RA Arredondo J., Grando S.A.;
RT "Cloning cholinergic receptors in human keratinocytes.";
RN Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
[7]
SEQUENCE OF 17-502 FROM N.A.
RP TISSUE=Brain;
RA Doucette-Stamm L., Monteggia L.M., Donnelly-Roberts D., Wang M.T.,
RA Lee J., Rian J., Giordano T.;
RT "Cloning and sequence of the human a7 nicotinic acetylcholine
RT receptor.";
RL Drug Dev. Res. 30:252-256(1993).
[8]
SEQUENCE OF 24-502 FROM N.A.
RP TISSUE=Retina;
RX MEDLINE=94245214; PubMed=8188270;
RA Chini B., Raimondi E., Elgoyhen A.B., Moralli D., Balzaretti M.,
RA Heinemann S.F.;
RT "Molecular cloning and chromosomal localization of the human alpha 7-
RT nicotinic receptor subunit gene (CHRNA7).";
RL Genomics 19:379-381(1994).
[9]
SEQUENCE OF 118-129 FROM N.A.
RP MEDLINE=21818878; PubMed=11829490;
RX Riley B., Williamson M., Collier D., Wilkie H., Makoff A.;
RT "A 3-Mb map of a large segmental duplication overlapping the alpha7-
RT nicotinic acetylcholine receptor gene (CHRNA7) at human 15q13-q14.";
RL Genomics 79:197-209(2002).
[10]
MASS SPECTROMETRY.
RP TISSUE=Breast cancer;
RX MEDLINE=21829512; PubMed=11840567;
RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA Zvelebil M.J.;
RT "Cluster analysis of an extensive human breast cancer cell line
RT protein expression map database.";
RL Proteomics 2:212-223(2002).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE AChR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-
CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY
```

CC CC SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- MASS SPECTROMETRY: MW=54157.68; METHOD=MALDI.

CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

CC -----

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CC -----

DR EMBL; X70297; CAA49778.1; -

DR EMBL; U40583; AAA83561.1; -

DR EMBL; U62436; RAB40114.1; -

DR EMBL; Y08420; CAA69697.1; -

DR EMBL; AF385585; AAK68111.1; -

DR EMBL; L25827; -; NOT_ANNOTATED_CDS.

DR EMBL; Z23141; CAA80672.1; -

DR EMBL; AF332758; AAK19515.1; -

DR PIR; G02259; G02259.

DR PIR; I37185; ACHUA7.

DR Genew; HGNC:1960; CHRNA7.

DR MIM; 118511; -

DR GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. . . ; TAS.

DR GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . . ; TAS.

DR GO; GO:000187; P:activation of MAPK; TAS.

DR GO; GO:0006832; P:small molecule transport; TAS.

DR InterPro; IPR006023; Neu_channel_memb.

DR InterPro; IPR006202; Neur_chan_LBD.

DR InterPro; IPR006201; Neur_channel.

DR Pfam; PF02931; Neur_chan_LBD; 1.

DR Pfam; PF02932; Neur_chan_memb; 1.

DR PRINTS; PR00252; NRIONCHANNEL.

DR TIGRFAMs; TIGR00860; LIC; 1.

DR PROSITE; PS00236; NEUOTR_ION_CHANNEL; 1.

DR Postsynaptic membrane; Ionic channel; Glycoprotein; signal;

DR Transmembrane; Multigene family.

FT SIGNAL 1 22

FT CHAIN 23 502

FT DOMAIN 23 230

FT TRANSMEM 231 255

FT TRANSMEM 262 280

FT TRANSMEM 296 317

FT DOMAIN 318 469

FT TRANSMEM 470 490

FT DISULFID 150 164

FT DISULFID 212 213

FT CARBOHYD 46 46

FT CARBOHYD 90 90

FT CARBOHYD 133 133

FT CONFLICT 11 11

FT CONFLICT 58 58

FT CONFLICT 134 134

FT CONFLICT 364 364

FT CONFLICT 375 375

FT CONFLICT 409 413

FT SEQUENCE 502 AA; 58449 MW; D94B3A482EAA0E42 CRC64;

Query Match 28.7%; Score 1159.5; DB 1; Length 502;

Best Local Similarity 45.1%; Pred. No. 1.le-73;

Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;

Qy 297 IYNLSAK---VCLAGYHEKRLHLDLDYNTLTPVNLSPVNSDPLQLSFGTLTMOIIDVDE 353

Db 8 VTLAASLHVSLSQGEFQKLYKELVKNPLRPVANDSQPLTVVLSLSLLQIMDVDE 67

Qy 354 KNOYLTNVWLKLEWDMNLRWNTSDYGGVKDRIIPPHRTWKPDVLMYNSADESGFDGTQ 413

Db 68 KNOYLTNWLQMSWTDHYLOWNVSEYPGVKTRFDPDQGIWKPDILLYNSADERFDFATFH 127

Qy 414 TNVVRNNGSCLYVPPGIFKSTCKIDITWTFPDDQRCRMKFGSWTYDGFOLDLQLODQETG 473

Db 128 TNVLNSSGHCQYLPPIGFKSSCYIDVRWPFDDVQHCKLAFGWSYGGWSLDLQMGE--- 184

Qy 474 GDISSVYLNGEWELLVGPGKRNELYYNCCPEPIDITFAIIIRRTLYYFNLIPCVLI 533

Db 185 ADISGYIPNGEWDLVGPGRSEFYECCKEYPDVDTFTVMRRRTLYYGLNLLIPCVLI 244

Qy 534 ASMALLCFTLPDPSGKLSIGVTLLASLTFLNVAETMPATSDAVPL----- 581

Db 245 SALALLVFLPADSGEKISLIGITVLLSLTFLMLVAEIMPATSDSVPLIAQYFASFTMIIV 304

Qy 582 -----WIRIVFLCWLPMILRMSRPG-----RPLILEFTTTP 612

Db 305 GLSVVTVTVIYLYHHHDPDGGKMPKWTIRVILLNCAWFLMKRPGEDKVRP-ACQHKQR 363

Qy 613 CSDTSSERKHQILSDVELKERSKSLANLVDIDDDDRH---NCRWMTGGTLPHNPAF 668

Db 364 CSLASVE-----MSAVAPPASNGNLLY-----IGRGLDGVHCVP-TP----- 401

Qy 669 YRTVYGGDDSGISGPIGSTRMPDAVTH-----HTCIKSSTEYELGLILKEIRFTDOLRK 723

Db 402 -----DSGVV-----CGMACSPHDEHLLHGGQPPEGDPDLAKLILEVRYIANFR 449

Qy 724 DDECNDIANDKFAAMVVDRLCLIIFTMFALIAVLVLSAPHII 768

Db 450 QDESEAVCSBWKFAACVVDRLCLMAFSVFTICTIGILMSAPNEV 494

RESULT 5

ACH7_BOVIN STANDARD; PRT; 499 AA.

ID ACH7_BOVIN PRT; 499 AA.

AC P54131;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neuronal acetylcholine receptor protein, alpha-7 chain precursor.

GN CHRNA7.

OS Bos Taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).

RC TISSUE=Adrenal medulla;

RA Garcia-Guzman M., Sala F., Sala S., Campos-Caro A., Stuehmer W.,

RA Gutierrez L., Criado M.;

RT "Alpha-Bungarotoxin-sensitive nicotinic receptors on bovine

RT chromaffin cells: molecular cloning, functional expression and

RT alternative splicing of the alpha 7 subunit.";

RL Eur. J. Neurosci. 7:647-655(1995).

CC -1- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN

CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND

CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA

CC MEMBRANE.

CC -1- SUBUNIT: FORMS A HOMO-OLIGOMERIC CHANNEL BLOCKED BY ALPHA-

CC BUNGAROTOXIN. THE STRUCTURE IS PROBABLY PENTAMERIC (BY

CC SIMILARITY). HOMO-OLIGOMER OF THE SHORT FORM GIVES RISE TO

CC UNFUNCTIONAL CHANNELS, AS DOES COEXPRESSION OF BOTH LONG AND SHORT

CC FORMS OF THE RECEPTOR.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- ALTERNATIVE PRODUCTS:

CC Event-Alternative splicing; Named isoforms=2;

CC Name=Long;

CC IsoId=P54131-1; Sequence=Displayed;

CC Name=Short;

CC IsoId=P54131-2; Sequence=VSP_000075;

CC -1- TISSUE SPECIFICITY: AT LEAST IN CHROMAFFIN CELLS.

CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.

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 DR EMBL; X93604; CAA63802.1; --
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_chan_memb.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRfams; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 499
 FT
 FT DOMAIN 20 227
 FT TRANSMEM 28 252
 FT TRANSMEM 259 277
 FT TRANSMEM 293 314
 FT DOMAIN 315 466
 FT TRANSMEM 467 487
 FT DISULFID 147 161
 FT DISULFID 209 210
 FT
 FT CARBOHYD 43 43
 FT CARBOHYD 87 87
 FT CARBOHYD 130 130
 FT VARSPIC 262 290
 FT
 FT SEQUENCE 499 AA; 56002 MW; AEE5D0B3820D4255 CRC64;

Query Match 28.6%; Score 1157; DB 1; Length 499;
 Best Local Similarity 46.4%; Pred. No. 1.7e-73;
 Matches 235; Conservative 76; Mismatches 122; Indels 74; Gaps 10;

QY 305 VCLAGYHEKRLHLLDLPYNTLRPVNLNESPLOLSFGLTLMQIIDVDEKQLLVTVNL 364
 DB 16 VSLQGEFQKLYKDLVKNYNPLRPVANDSLPTVYFSLQLQIMDYDEKQVLTNIWL 75
 QY 365 KLEWDMNLRWNTSDYGVGKDLRPPHRIKWPDLVMTNSADEGFGDTGTQTVNVVNRNGSC 424
 DB 76 QMTWTDHYLQWNASEYFGVKTVRFPDGOIWKPDILLNSADEREDATFTNVLNMSGHC 135
 QY 425 LYVPPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFQDLQQLQDETGGDISSYVLNGE 484
 DB 136 QYLPPIGIFKSSCYIDVRWFPDQVQCKLFGFSWYGGWSLDLQOE---ADISGYIPNGE 192
 QY 485 WELGVGPKRNEIYNCPEYIDITAIIRRTLYFFNLIIPCVLISALLGTTLP 544
 DB 193 WDLVGLGKSRKEFYECCKEYPPDVTETVTSRRRTLYGLNLLPCVLISALLVLLFP 252
 QY 545 PDSGEKLSLGVITLLSTVFLNVAETMPATSDAVPL----- 581
 DB 253 ADSGEKLSLGVITLLSTVFLNVAETMPATSDVPLIAQYFASTMIIVGLSVVTVIVL 312
 QY 582 -----WIRIVLCWPLWILRMSRGRPLILEFPTTSCDTSERKHQLSD 627
 DB 313 QYHHDPDGGKMPKWTWVLLNCAWFLRMKRPQ-----EDKVPACQHNRRCSS--LAS 365
 QY 628 VELKE-RSSKSLANVLIDIDDDFR-----HNCPRMTPGTLPHNPAFTVYVGGDDGSI- 681
 DB 366 VEMSAVAGPATNGNLLYI--GFGLDTHMCAV-TP-----DSGWC 404
 QY 682 GPIGSTRMPDAVTHHTCKISTEYELGLILKEIFITDOLRKDCDNDIANDWKFAMVY 741
 DB 405 GRVACSTHDEHLLHAGQSGDDPLAKILLEEVYIAHRFCQDESAVCSWKFAACV 464

QY 742 DRLCLIIFTFAIATIAVLASAPHII 768
 DB 465 DRLCLMAFSVFTILCTIGILMSAPNFV 491

RESULT 6

ACHL_CAEEL STANDARD; PRT; 498 AA.
 ID AC1_CAEEL
 AC P48180;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Acetylcholine receptor like protein, alpha-type chain precursor.
 GN F25G6.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RX MEDLINE=96196478; PubMed=8627624;
 RA Ballivet M., Alliod C., Bertrand S., Bertrand D.;
 RT "Nicotinic acetylcholine receptors in the nematode *Caenorhabditis*
 RL *elegans*."; J. Mol. Biol. 258:261-269(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Nelson J., Wohlmann P.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: POSSIBLE ACETYLCHOLINE RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 DR EMBL; X83887; CAA58764.1; --
 DR PIR; S68588; S68588.
 DR HSP; P58154; 119B.
 DR WormPep; F25G6.3; CE09639.
 DR InterPro; IPR006029; Neu_chan_memb.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR InterPro; IPR006201; Neur_chan_memb.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 DR Pfam; PF02932; Neur_chan_memb; 1.
 DR PRINTS; PR00252; NRIONCHANNEL.
 DR TIGRfams; TIGR00860; LIC; 1.
 DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
 KW Transmembrane; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 498
 FT
 FT DOMAIN 20 230
 FT TRANSMEM 231 252
 FT TRANSMEM 261 279
 FT TRANSMEM 295 314
 FT DOMAIN 315 472
 FT TRANSMEM 473 493
 FT DISULFID 147 161
 FT DISULFID 211 212
 FT
 FT CARBOHYD 43 43
 FT CARBOHYD 93 93

POTENTIAL.
 ACETYLCHOLINE RECEPTOR LIKE PROTEIN,
 ALPHA-TYPE CHAIN.
 EXTRACELLULAR (POTENTIAL).
 POTENTIAL.
 POTENTIAL.
 POTENTIAL.
 POTENTIAL.
 CYTOPLASMIC (POTENTIAL).
 POTENTIAL.
 BY SIMILARITY.
 ASSOCIATED WITH RECEPTOR ACTIVATION
 (BY SIMILARITY).
 N-LINKED (GLCNAC. . .) (POTENTIAL).
 N-LINKED (GLCNAC. . .) (POTENTIAL).

DR Pfam: PF02931; Neur_chan_LBD; 1.
DR Pfam: PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 567
FT DOMAIN 22 240
FT TRANSMEM 241 264
FT TRANSMEM 272 290
FT TRANSMEM 306 325
FT DOMAIN 326 513
FT TRANSMEM 514 532
FT DISULFID 149 163
FT DISULFID 222 223
FT CARBOHYD 45 45
FT CARBOHYD 233 233
FT VARIANT 538 538
FT CONFLICT 108 108
SQ SEQUENCE 567 AA; 64019 MW; 08EIF721FB2A92AC CRC64;
Query Match 22.0%; Score 888; DB 1; Length 567;
Best Local Similarity 35.2%; Pred. No. 1.3e-54;
Matches 196; Conservative 91; Mismatches 168; Indels 102; Gaps 10;
QY 291 SWIFLLIYNLS-AKVCAGYHEKRLHLLDPYNTLPRVNLNEDSPLQLSFGLTLMQII 349
Db 3 SYLFAVFTALHFGGLGPAKRLYDILLNRYNRLIRPVGNNSDRIVTKMGLRLSLQI 62
QY 350 DYDEKNQLLVTVNWLKLEWDMNLRWNTSDYGVKDLRIPPHRWKPDVLMVNSADEGD 409
Db 63 DYNLNQINMTNWEQENDYKLNWPDYGVDTLHVPSEHILWPLDIVLNADGNYE 122
QY 410 GYQYNNVVRNNGSLVPPGIFKSTCKIDITWFFPDQRCCKGWSYDGFOLDL--- 466
Db 123 VTIMTKAILHRTGKVVWKPPIAYKSCFEDVEYFPDEQTCFMKFGSWTYGYMVDLRL 182
QY 467 -QLQD---ETGDSLVVNGEWELLVGPGRNELIYNCCPEYIDITFAIIIRRTLY 521
Db 183 KOTASDNEVGIDLDYIYSVWDMIRVAVRNEKFKYSCCEPDIIVNLTLRKTLF 242
QY 522 YFNLIIPCVLIASMLLFTLPDPSGKSLGVTLLSLTVFLNNVAETPATSDAVPL 581
Db 243 YTVNLIIPCVGISFLSVLYPLSDSGEKISLISILLSTVFFLLAEIIPPTSITVPL 302
QY 582 -----WIRIVFLCWLPIWRMSRGRPL 604
Db 303 LGKYLFTMLVTLVVVYIAVLNVRSPVTHRMAPWVQRLFIQLPKLICIERPKK-- 360
QY 605 ILEFPTPCSDTSRKKQILSDV-ELKERSKSLANVLDIDDDFRHNCRPMTPGGTLP 663
Db 361 -----EPEEDQPPVLTVDVHLPP-----DVDKFNVDKRFSGDYGP 400
QY 664 HNPAYR-----TVYGGDD-----GSIGPTGSTRMPDAVTH 695
Db 401 ALPASHRFDLAAAGTSAHCAFPPLPSLPLPGADDDLFSPSLGNGDISPCCPAAAAA 460
QY 696 HFCIKSST-----EYELGLILKEIRFITDLRKDDCNDIANDWFAAMVDRCLLIIFT 750
Db 461 AAADLSPTFKPYAREMKTIEGSRFIAHQVANKKFKFESVEDWYVAMVLDLRFMTWIFA 520
QY 751 MEAILATIAVLISAPHI 767
Db 521 IACVVGTAIIILQAPSL 537
PRT; 516 AA.
RESULT 8
ACH1_MANSE STANDARD; PRT; 516 AA.
ID ACH1_MANSE

AC DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholine receptor protein, alpha-like chain precursor (MARAL).
GN ARAL.
OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
OC Spingidae; Sphinginae; Manduca.
OX NCBI_TaxID=7130;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98424077; PubMed=9753155;
RA Eastham H.M., Lind R.J., Eastlake J.L., Clarke B.S., Townner P.,
RA Reynolds S.E., Wolstenholme A.J., Wonnacott S.;
RT "Characterization of a nicotinic acetylcholine receptor from the
insect Manduca sexta";
RL Eur. J. Neurosci. 10:879-889(1998).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: Y09795; CAA70928.1;
DR InterPro: IPR006029; Neur_chan_memb.
DR InterPro: IPR006202; Neur_chan_LBD.
DR InterPro: IPR006201; Neur_chan.
DR Pfam: PF02931; Neur_chan_LBD; 1.
DR Pfam: PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 21
FT CHAIN 22 516
FT DOMAIN 22 243
FT TRANSMEM 244 264
FT TRANSMEM 274 294
FT TRANSMEM 306 326
FT DOMAIN 327 465
FT TRANSMEM 466 486
FT DISULFID 149 163
FT DISULFID 222 223
FT CARBOHYD 45 45
FT CARBOHYD 132 132
FT CARBOHYD 233 233
SQ SEQUENCE 516 AA; 58720 MW; E7A71E8C45D13BD2 CRC64;
Query Match 21.9%; Score 886; DB 1; Length 516;
Best Local Similarity 36.6%; Pred. No. 1.5e-54;
Matches 199; Conservative 65; Mismatches 141; Indels 138; Gaps 9;
QY 298 YLN---LSAKVCLAGYHEKRLHLLDPYNTLPRVNLNEDSPLQLSFGLTLMQIIDVDEK 354
Db 8 YLHGVLVFLATGAGNPDARLKYDLLSNKLVRLVPLNVSDALTVRIKLSQLIDVNLK 67
QY 355 NQLLVTVNWLKLEWDMNLRWNTSDYGVKDLRIPPHRWKPDVLMVNSADEGFGDTQT 414
Db 68 NQIMTTLNWEQSWDYKLSWEPREYGGVEMLHVPDHLWRPDIVLYNNADGNFEVTLAT 127

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Qy 415 NVVNRNGSLVPPGIFKSTCKIDITWFFDQRCMKFGSWTYDGFOLDLQDETGG 474
Dy 128 KATLNYTGRVWEPRPAIYKSSCEIDVEYFPDQDQTCVMKFGSWTYDGFQVLDLHIDEVRG 187
Qy 475 -----DISSVYLVNGEWELLGVGKRNIEIYNCCPEPIDITFAIIRRTLYFFNL 526
Dy 188 TNVVELGVDLSEFYTSVEMDILEYPAVRNEKFYTCDEPYDIDITFNITMRKTLFTYVNL 247
Qy 527 IIPCVLIASMALLGFTLPPDSGEKLSGVTLISLVFLNVAETMPATSDAVPL----- 581
Dy 248 IIPCMGISFTLVLYLPDSGKVSLSISILSLTVFFLLAEIIPPTSLVPLLGKVF 307
Qy 582 -----WIRIVFLCWLPMILRMSRPGRLILEFP 609
Dy 308 LFTMILDTFSICVTVVNLNVHFRSPQHTMSPVWRVFIHVLPRLLVMRRP----- 358
Qy 610 TTPCSDPSSERKHOILSDVELKERSSKSLANVLIDIDDDFRHNCRPMTPCGTILPHNPAFY 669
Dy 359 -----HYRLD-----PHRSRFA 370
Qy 670 RTVYGOG-----DGSIGPIGSTRMP-----DAVTH-HTCIKSS 702
Dy 371 GLVTGAGETLWDGSGVGPVAPPPPCAPPLAPCAACAPAEAPALCDALRRHRC----- 426
Qy 703 TEVELGLILKEIRFITDQLRKDDCNDIANDWKFAMVVDRLCLLIIFTMFAILATIAVLL 762
Dy 427 --PELHKAIDGINYADQTRKEESTRVKEDWKVYAMVLDRLPFLWIFTLAVVVGSAIGIL 484
Qy 763 SAP 765
Dy 485 QAP 487

RESULT 9
ID ACHI_SCHGR STANDARD; PRT; 557 AA.
AC P23414;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholine receptor protein, alpha-L1 chain precursor.
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Cyrtacanthacridinae; Schistocerca.
OX NCBI_TaxID=7010;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91092263; PubMed=1702381;
RA Marshall J., Buckingham S.D., Shingai R., Lunt G.G., Goosey M.W.,
RA Darlison M.G., Sattelle D.B., Barnard E.A.;
RT "Sequence and functional expression of a single alpha subunit of an
RT insect nicotinic acetylcholine receptor.";
RL EMBO J. 9:4391-4398(1990).
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X55439; CAA39081.1; -
DR PIR; S12359; S12359.
DR InterPro; IPR006029; Neu_channel_memb.
```

```
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PR00252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; signal;
KW Transmembrane; Multigene family.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 557 ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-L1
FT DOMAIN 24 244 EXTRACELLULAR.
FT TRANSMEM 245 266
FT TRANSMEM 274 294
FT TRANSMEM 308 329
FT DOMAIN 330 500 CYTOPLASMIC.
FT TRANSMEM 501 523
FT DISULFID 151 165
FT DISULFID 224 225
FT CARBOHYD 47 47 BY SIMILARITY.
FT CARBOHYD 235 235 ASSOCIATED WITH RECEPTOR ACTIVATION
FT DOMAIN 382 400 (BY SIMILARITY).
FT DOMAIN 406 422 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DOMAIN 406 422 ALA/SER-RICH.
FT SEQUENCE 557 AA; 63026 MW; 168389C887DFDF3E CRC64;
HIS-RICH.

Query Match 21.6%; Score 873; DB 1; Length 557;
Best Local Similarity 36.8%; Pred. No. 1.4e-53;
Matches 197; Conservative 90; Mismatches 174; Indels 74; Gaps 8;

Qy 293 IFLLIYNLSAKVCLAGYHEKRLHLLDLPNTLERVNLSDPLQLSFGTLMQIIDVD 352
Dy 8 MLLLLLLLLLHPAAANPDAAKRLYDLLSNVNLIRPVSNNITDVLVKGILGRLSOLIDLN 67
Qy 353 EKNOLLVTNWLKLEWDMNMLRWNTSDYGVGKOLRIPPHRIKWPDVLMYNSADGFGTY 412
Dy 68 LKQILTTNWLHEWQDHKEFRMDPAEYGVGTELYSEHILWPLDIYLNADGEYVYTT 127
Qy 413 QTNVVRNGSLVPPGIFKSTCKIDITWFFDQRCMKFGSWTYDGFOLDL-----QL 468
Dy 128 MTRAVLHHTGKVWVTPPAIFKSCSIDVRYFPDQDQTCVMKFGSWTYDGFOLDLKHINQK 187
Qy 469 QDE-----TGGDISYVLNGEWELLGVGKRNIEIYNCCPEPIDITFAIIRRTLYYFF 524
Dy 188 YDDNKVKVGIDLREYVPSVEMDILGVAERHEKYPCCAEYPDIFENITLRKTLFTYV 247
Qy 525 NLIIPCVLIASMALLGFTLPPDSGEKLSGVTLISLVFLNVAETMPATSDAVPL--- 581
Dy 248 NLIIPCVLISVLYSVLYPADSGEKIALCISILLSTQTMFLFLLISEIPTSLALPLGK 307
Qy 582 -----WIRIVFLCWLPMILRMSRPGRLILE 607
Dy 308 YLLFTVWLVGLSVVITMVLNVHYRKFTSKHMAPVRKVFIRRLPKLLMRVPEQLL--- 364
Qy 608 FPTTPCSDTSSERKHOILSDVELKERSSKSLA-----NVLIDDDFRHN----- 652
Dy 365 -----ADLASKRLRLRAHNSKLSAAAAAASSSAASSPSDLRHHHLHQHQHHL 418
Qy 653 --CRPMPGCTLPHNPAFYTYVYGDDGSGIGPIGSTRMPDPAVTHHTCIKSSYEYELGLI 710
Dy 419 QLHHLQRPGGCNGLSATNR--FG-GSAGAGFGLPSVVGDLGSLSDVATRKRYFELEKA 475
Qy 711 LKEIRFTDOLRKDDCNDIANDWKFAMVVDRLCLLIIFTMFAILATIAVLLSAP 765
Dy 476 IHNVLFIQNHMQRODEDAEDQDQMGFVAMVLDRLFLWIFTLFIATISVGTFAILCEAP 530

RESULT 10
ID ACHI_HUMAN STANDARD; PRT; 529 AA.
AC Q15822; Q9HQA03;
DT 01-NOV-1997 (Rel. 35, Created)
```

DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-2 chain precursor.
 GN CHRNA2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=97062879; PubMed=8906617;
 RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
 RA Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
 RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
 RT 2-beta 4 nicotinic acetylcholine receptor subunits and functional
 RT expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
 RT beta 4 subunits";
 RL J. Mol. Neurosci. 7:217-228(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Groot Kormelink P.J.;
 RX Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RA [3]
 RP SEQUENCE FROM N.A.
 RC Brechtshmidt K., Rosenthal A.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPES
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA). ALPHA-2 SUBUNIT CAN BE
 CC COMBINED TO BETA-2 OR BETA-4 TO GIVE RISE TO FUNCTIONAL RECEPTORS.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC
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 CC
 DR EMBL: U62431; AAB40109.1; -;
 DR EMBL: Y16281; CAA76154.1; -;
 DR EMBL: AF311103; -, NOT_ANNOTATED_CDS.
 DR Genew: HGNC:1956; CHRNA2.
 DR MIM: 118502;
 DR GO: GO:0003892; C:nicotinic acetylcholine-gated receptor-chan. . . ; TAS.
 DR GO: GO:0004889; F:nicotinic acetylcholine-activated cation-se. . . ; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR GO: GO:0007268; P:synaptic transmission; TAS.
 DR InterPro: IPR006029; Neur_chan_memb.
 DR InterPro: IPR006201; Neur_chan_LBD.
 DR Pfam: PF02931; Neur_chan_LBD; 1.
 DR Pfam: PF02932; Neur_chan_memb; 1.
 DR PRINTS: PRO0252; NRIONCHANNEL.
 DR TIGRFAMS: TIGR00860; LIC; 1.
 DR PROSITE: PS00236; NEUROTR_ION_CHANNEL; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 KW Transmembrane; Multigene family.
 FT SIGNAL 1 26
 FT CHAIN 27 529 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 FT DOMAIN 27 264 ALPHA-2 CHAIN.
 FT TRANSMEM 265 289 EXTRACELLULAR.
 FT TRANSMEM 297 315 POTENTIAL.
 FT TRANSMEM 331 352 POTENTIAL.
 FT DOMAIN 353 502 CYTOPLASMIC.
 FT TRANSMEM 503 521 POTENTIAL.

FT DISULFID 183 197 BY SIMILARITY.
 FT DISULFID 247 248 ASSOCIATED WITH RECEPTOR ACTIVATION
 FT (BY SIMILARITY).
 FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 125 125 A -> T (IN REF. 3).
 SQ SEQUENCE 529 AA; 59735 MW; 7F512B06CDD9AAEF CRC64;
 Query Match 21.0%; Score 848.5; DB 1; Length 529;
 Best Local Similarity 36.7%; Pred. No. 6.6e-52;
 Matches 183; Conservative 87; Mismatches 154; Indels 75; Gaps 10;
 QY 309 GYH---EKRLHDLDPYNTLERYLNESDPQLSFLGLTLMQIIDVDENQLLVNVLK 365
 DB 53 GSHTETEDRLPKHFRGYNWRARPVNTSDVIVRFGLSIAOLIDVDENKMMTNNVLK 112
 QY 366 LEWMDNLRWNTSDYGGVKDLRIPHRITKWPVLMYNSADEGFDGTQTNVVRNNGSL 425
 DB 113 QEMSDYKLRWNPADFGNITSLRVPSEMIWIPDIVLYNNADGEFAVHTMTKAHLFGTGVH 172
 QY 426 YVPPGIFKSTCKIDITWPFDDORCEMKFGSWTYDGFOLDLQDETGGDISSYVLNGEW 485
 DB 173 WVPPIAYKSSCIDVTFPPFDQONCKMKFGSWTYDKAKIDLEQMEQT-VLDKYWESGEW 231
 QY 486 ELLGVPGKRNEIYNCCEPEYIDITFAIIIRRTLYFFNLIIPCVLIASMAALLFTLPP 545
 DB 232 AIVNATGYNSKKYDCCAEIYDVYAFVIRLPLFYTLINLIIPCLLSLVLVLP 291
 QY 546 DSGEKSLGVITLLSLTVFLNMVAETMPATSDAVL----- 581
 DB 292 DCGEKITLISVLLSLTVFLNLIITPISLVIPLIGEYLLFTMFVTLSTIVTFVLN 351
 QY 582 -----WIRIVFLWLPWLRMSRGRPLILEFTPTPCSDTSSERKHOLISDV 628
 DB 352 VHRSPSTHTWVRGALLGCVPRWLLMNRPPPEL---CHPLRLKLSPSYHWLESV 408
 QY 629 ELKERSKSLANLVIDDDFRHNCR-PMTPG-GTLPHNPAFYRTVYQGDDSGSIGPIGS 686
 DB 409 DAEERE-----VVVEEDRWACAGHAVPSVGLT-----CSHGLHSGASGPRAE 452
 QY 687 TRMPDA---VTHHTCIKSTVEYELGLILKEIRFTDOLRKDECDNDKFAAMVVD 743
 DB 453 ALLQEGELLSPH-----MOKALEGVHYIADLRSEADSDSVKEDMKYVAMVIDR 502
 QY 744 LCLIFTMFAIATIAVL 762
 DB 503 IFLWLFIIIVCFGTIGLFL 521
 RESULT 11
 ACH3_HUMAN
 ID ACH3_HUMAN STANDARD; PRT: 503 AA.
 AC P32297; Q15823; Q96RH3; Q99553; Q9BQ93;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neuronal acetylcholine receptor protein, alpha-3 chain precursor.
 GN CHRNA3 OR NACHRA3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90245296; PubMed=2336208;
 RA Fornasari D., Chini B., Tarroni P., Clementi F.;
 RT "Molecular cloning of human neuronal nicotinic receptor alpha
 RT 3-subunit.";
 RL Neurosci. Lett. 111:351-356(1990).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Thymus;

RX MEDLINE-91114756; PubMed-1989896;
 RA Mihovilovic M., Roses A.D.;
 RT "Expression of mRNAs in human thymus coding for the alpha 3 subunit
 of a neuronal acetylcholine receptor.";
 RL Exp. Neurol. 111:175-180(1991).
 [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE-97062879; PubMed-8908617;
 RA Elliott K.J., Ellis S.B., Berckhan K.J., Urrutia A.,
 Chavez-Noriega L.E., Johnson E.C., Velicelebi G., Harpold M.M.;
 RT "Comparative structure of human neuronal alpha 2-alpha 7 and beta
 2-beta 4 nicotinic acetylcholine receptor subunits and functional
 expression of the alpha 2, alpha 3, alpha 4, alpha 7, beta 2, and
 beta 4 subunits.";
 RL J. Mol. Neurosci. 7:217-228(1996).
 [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE-97162233; PubMed-9009220;
 RA Groot Kormelink P.J., Luyten W.H.M.L.;
 RT "Cloning and sequence of full-length cDNAs encoding the human neuronal
 nicotinic acetylcholine receptor (nAChR) subunits beta3 and beta4 and
 expression of seven nAChR subunits in the human neuroblastoma cell
 line SH-SY5Y and/or IMR-32.";
 RL FEBS Lett. 400:309-314(1997).
 [5]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE-99118870; PubMed-9921897;
 RA Rempel N., Heyers S., Engels H., Slegers E., Steinlein O.K.;
 RT "The structures of the human neuronal nicotinic acetylcholine receptor
 beta2- and alpha3-subunit genes (CHRNA2 and CHRNA3).";
 RL Hum. Genet. 103:645-653(1998).
 [6]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE-21342809; PubMed-11450844;
 RA Lev-Lehman E., Bercovich D., Xu W., Stockton D.W., Beaudet A.L.;
 RT "Characterization of the human beta4 nAChR gene and polymorphisms in
 CHRNA3 and CHRNA4.";
 RL J. Hum. Genet. 46:362-366(2001).
 [7]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX TISSUE=Lung;
 MEDLINE-22388257; PubMed-12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [8]
 RP SEQUENCE OF 30-503 FROM N.A.
 TISSUE=Brain;
 RA Anand R., Lindstrom J.;
 RL Submitted (JUN-1990) to the EMBL/GenBank/DBJ databases.
 [9]
 RP SEQUENCE OF 6-493 FROM N.A.
 TISSUE=Epidermal keratinocytes;
 RA Arredondo J., Grando S.A.;
 RT "Cloning cholinergic receptors in human keratinocytes.";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
 CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
 CC LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
 CC MEMBRANE.
 CC -!- SUBUNIT: NEURONAL ACHR SEEMS TO BE COMPOSED OF TWO DIFFERENT TYPE
 CC OF SUBUNITS: ALPHA AND NON-ALPHA (BETA).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P32297-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P32297-2; Sequence=VSP_000073;
 CC Note=No experimental confirmation available;
 CC SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNEL FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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 CC -----
 CC EMBL; M86383; AAC84176.1; -;
 CC EMBL; M37981; AAA59942.1; -;
 CC EMBL; U62432; AAB40110.1; -;
 CC EMBL; Y08418; CAA69695.1; -;
 CC EMBL; AJ007783; CAA07682.1; -;
 CC EMBL; AJ007784; CAA07682.1; JOINED.
 CC EMBL; AJ007785; CAA07682.1; JOINED.
 CC EMBL; AJ007786; CAA07682.1; JOINED.
 CC EMBL; BC001642; AAH01642.1; -;
 CC EMBL; BC002996; AAH02996.1; -;
 CC EMBL; BC000513; AAH00513.1; -;
 CC EMBL; AF385584; AAK68110.1; -;
 CC EMBL; X53559; CAA37625.1; -;
 CC PIR; A37040; A37040.
 CC PIR; A53956; A53956.
 CC Genew; HGNC:1957; CHRNA3.
 CC MIM; 118503; -;
 CC GO; GO:0005892; C:nicotinic acetylcholine-gated receptor-chan. . . ; TAS.
 CC GO; GO:0004889; F:nicotinic acetylcholine-activated cation-se. . . ; TAS.
 CC GO; GO:0005215; F:transporter activity; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC GO; GO:0006832; P:small molecule transport; TAS.
 CC InterPro; IPR006039; Neu_chan_memb.
 CC InterPro; IPR006202; Neu_chan_LBD.
 CC InterPro; IPR006201; Neur_channel.
 CC Pfam; PF02931; Neur_chan_LBD; 1.
 CC Pfam; PF02932; Neur_chan_memb; 1.
 CC PRINTS; PR00252; NRIONCHANNEL.
 CC TIGRfams; TIGR00860; LIC; 1.
 CC PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
 CC Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
 CC Transmembrane; Multigene family; Alternative splicing; Polymorphism.
 CC SIGNAL 1 29 POTENTIAL.
 CC CHAIN 30 503 NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN,
 CC ALPHA-3 CHAIN.
 CC DOMAIN 30 238 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 239 263 POTENTIAL.
 CC TRANSMEM 271 289 POTENTIAL.
 CC TRANSMEM 305 326 POTENTIAL.
 CC DOMAIN 327 475 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 476 495 POTENTIAL.
 CC DISULFID 157 171 BY SIMILARITY.
 CC DISULFID 221 222 ASSOCIATED WITH RECEPTOR ACTIVATION
 CC (BY SIMILARITY).
 CC CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC VARSPPLIC 1 5 MALAV -> MGSGPL (in isoform 2).
 FT /FTid=vsp_000073.

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FT VARIANT      21      21      L -> LL.
FT CONFLICT      5      13      /FTIG-Var_013240.
FT CONFLICT     11      14      LSPP -> CRA (IN REF. 1).
FT CONFLICT     100     100      D -> G (IN REF. 1).
FT CONFLICT     132     133      DD -> TT (IN REF. 1).
FT CONFLICT     235     235      I -> S (IN REF. 1).
FT CONFLICT     430     430      L -> V (IN REF. 1).
SQ SEQUENCE     503 AA; 57309 MW; 8A9EBBC5D71AEC7D6 CRC64;

Query Match
Best Local Similarity 35.2%; Score 845; DB 1; Length 503;
Matches 178; Conservative 97; Mismatches 166; Indels 64; Gaps 6;

QY 295 LIYINLSAKVCLAGYHEKRLHLDLPYNTLERPVNLNEDPLQLSFGTLTMOIIVDVRK 354
DB 17 LLLLLL-LPVARASEAERHLERFLFEDYNIIRPVANVSDPVIIFEVMSQLVKVDEV 75

QY 355 NOLLVTNWLKLEWDMNLRWNTSDYGGVKDLRIIPHRILWKPDVLMYNSADEGFDGTQY 414
DB 76 NQIMETNMLKQIWDYKUKWNPDSYGGAEFMRVPAQKIWKPDVLYNNNAVGFQVDDKT 135

QY 415 NYVVRNNGSCLYVPPGIFKSTCKIDITWPPDDQRCMKFGSWTVDGFDOLDLQDQETGG 474
DB 136 KALLKTYGVTWIPPAIFKSSCKIDVYPPDYQNCYMKFGSWYDKAKIDLVLIG-SSM 194

QY 475 DISSVNLGEWELLGVPGKRNIIYVNCPEPIDITFAIIIRRLIYFFNLIIPCVLIA 534
DB 195 NLKDYWESGEWAIKAPGYKHDIKYNCCBEIYDPDITSLYIRRLPLFTYINLIICLLAIS 254

QY 535 SMALLGFTLPPDSGKLSGVTLISLTVFLNVAETMPATSDAVPL----- 581
DB 255 FTVLVFLYPSDCGEKVLICISVLLSLTVFLVLTITPSTSLVPLIGEYLLFTWIFVT 314

QY 582 -----WIRVFLCWLFWILMRSPGRPLILEFPTTPCSDTS 617
DB 315 LSIVITVFLNVHYRTPTHTPMSWKTFLNLLPRV-----FWTRPTSNEG 362

QY 618 SERKHIQLSDVELKERSKSLANVLIDDDFRHNCRPMTPGGLPHNPAFRTVYGGQD 677
DB 363 NAQKRPRLYGAELSNLNCFSRAES-----KGCKEGYPCQDGMCGYCHRRRIKISNF 413

QY 678 DGSIGPIGSTRMPDAVTHTCIKSSTVEYELGILILKEIRFITDQLRKDDCNDIANDWKA 737
DB 414 SANLFRSSSESVDVLS-----LSALSPKAIQSVKVIENAKQAEKIQDDWKV 469

QY 738 AMVDRLCLIIFTFAILATIAVL 762
DB 470 AMVIDRIFLWVFLVCLILGTAGLFL 494

RESULT 12
ACH2_DROME
ID ACH2_DROME STANDARD; PRT; 576 AA.
AC P17644; Q9VC73;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acetylcholine receptor protein, alpha-like chain 2 precursor.
GN NACR-ALPHA-96AB OR ACR96AB OR SAD OR ACR96AB OR CG5844.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Head;
RX MEDLINE=90301489; PubMed=2114015;
RA Baumann A., Jonas P., Gundelfinger E.D.;
RT "Sequence of D alpha 2, a novel alpha-like subunit of Drosophila
RT nicotinic acetylcholine receptors.";
RL Nucleic Acids Res. 18:3640-3640(1990).

[2]
SEQUENCE FROM N.A.
TISSUE-Head;
RX MEDLINE=90353591; PubMed=2117557;
RA Jonas P., Baumann A., Merz B., Gundelfinger E.D.;
RT "Structure and developmental expression of the D alpha 2 gene
RT encoding a novel nicotinic acetylcholine receptor protein of
RT Drosophila melanogaster.";
RL FEBS Lett. 269:264-268(1990).
[3]
SEQUENCE FROM N.A.
MEDLINE=90360975; PubMed=1697262;
SAWRUK E., Schloss P., Betz H., Schmitt B.;
RT "Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD,
RT a novel developmentally regulated alpha-subunit.";
RL EMBO J. 9:2671-2677(1990).
[4]
SEQUENCE FROM N.A.
STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew K.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadiou E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwack C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
[5]
SEQUENCE FROM N.A.
STRAIN=Berkeley; TISSUE=Head;
RC Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuncio J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: CNS IN EMBRYOS.

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Query Match
Best Local

Search completed: August 13, 2003, 15:26:10
Job time : 19.1234 secs

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DR EMBL; X12435; CAA30282.1; JOINED.
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DR EMBL; X07335; CAA30282.1; JOINED.
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DR EMBL; AF051909; AAC06012.1; -.
DR EMBL; M14808; AAA48565.1; -.
DR EMBL; M14809; AAA48564.1; -.
DR PIR; I50150; I50150.
DR PIR; S00376; ACCHAN.
DR InterPro; IPR006029; Neu_channel_memb.
DR InterPro; IPR006202; Neur_chan_LBD.
DR InterPro; IPR006201; Neur_channel.
DR Pfam; PF02931; Neur_chan_LBD; 1.
DR Pfam; PF02932; Neur_chan_memb; 1.
DR PRINTS; PRO0252; NRIONCHANNEL.
DR TIGRFAMS; TIGR00860; LIC; 1.
DR PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW Transmembrane.
FT SIGNAL 1 20
FT CHAIN 21 456
FT DOMAIN 21 229
FT TRANSMEM 230 254
FT TRANSMEM 262 280
FT TRANSMEM 296 315
FT DOMAIN 316 427
FT TRANSMEM 428 446
FT DISULFID 147 161
FT DISULFID 211 212
FT CARBOHYD 160 160
FT CONFLICT 33 33
SQ SEQUENCE 456 AA; 52183 MW; 0B31B6EABD7B4D42 CRC64;

Query Match 20.5%; Score 827.5; DB 1; Length 456;
Best Local Similarity 34.6%; Pred. No. 1.6e-50;
Matches 176; Conservative 92; Mismatches 130; Indels 111; Gaps 12;

QY 293 IFLLIYLNLSARVCLAGYHEKRLHLDLPYNTLPRVPLNESDPLQLSFGITLMOIIDVD 352
Db 6 VLLIFSAAGPALCYE--HETRLVDLDFREYSKVVPRPVENHRDVAVVTVGLIQLINVD 63
QY 353 EKNQLLVNTVWKLWENDMNLRWNTSDYGGVKDLRIPIPHRIWKDPVLMYNSADEGFGTY 412
Db 64 EVNQIVTTNVRLLKQWTDINLKWPNDDYGGVKQIRIPSDDIWRPDLVLYNNADGFAIVK 123
QY 413 QTNVVRNNGSCLVPPGIFKCKIDITWPEDDQRCMKFGSWTYDGFOLDLOQDET 472
Db 124 YTKVLLHTGTITWTPPAIFKSYCEIIVYFPDQNCMKLGTWTDGTWVVPINPESDR 183
QY 473 GGDISSYVLNGEWELLGVGKRNEIYYNCCPE-PYIDITFAIIIRRTLYFFNLIIPCV 531
Db 184 -PDLNFMESGEWYMKDYRGWKHWYVYACCPDTPYLDITYHFLMQLPLFYIVNVIIPCL 242
QY 532 LIASWALLGFTLPDPSGKLSGLVTILLSLVFLNMVAETMPATSDAVPL----- 581
Db 243 LFSFLTGFVFLPTDSGEKMTLSVLLSLVFLVIVELIPSTSSAVPLIGKYMLETWV 302
QY 582 -----WIRIVELCWLPIIL---RMSRPGRLILEPTT 611
Db 303 FVIASIIITVIVINTHRSPSTHTMPWPWRKIFIDTIPNIMFFSTMKRPSR----- 353
QY 612 PCSDTSSERKHQILSDVELKERSKSLLANVLDIDDDFRHNCRPMTPGGTLPHNPAFYRT 671
Db 354 -----DKPDKKIFAEDIDISEICKQ-----GpVPVN--FY-- 382
QY 672 YVGQDDGSGIGPSTRMPDVAHTHTCKISSTYELGLILKEIRFITDQLRKDDCECDIA 731
Db 383 -----SPL--TKNPD-----VKNAIE-----GIRYIAETMKSDQESSNAA 415
QY 732 NDWKFAAMVDRLCLIIFTMEFALITAV 760
Db 416 DEWKFVAMVLDHLLVIFMLVICITGLAV 444
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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:21:45 ; Search time 28.7606 Seconds
(without alignments)
2574.698 Million cell updates/sec

Title: US-09-303-232-2
Perfect score: 4043
Sequence: 1 MNAQKLFEVDDELWLAV.....MFAITATIAVLISAPHIIVS 770

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1182.5	29.2	502	2 A57175	nicotinic acetylch
2	1179.5	29.2	502	2 JN0113	nicotinic acetylch
3	1173.5	29.0	502	2 T01378	nicotinic acetylch
4	1168	28.9	511	2 JH0173	alpha-bungarotoxin
5	1160.5	28.7	502	1 ACH0A7	nicotinic acetylch
6	1155.5	28.6	502	2 G02259	alpha 7 neuronal n
7	1104	27.3	498	2 S68588	nicotinic acetylch
8	1009.5	25.0	461	2 T25671	hypothetical prote
9	988	24.4	560	2 T19622	hypothetical prote
10	968.5	24.0	542	2 T19622	hypothetical prote
11	889	22.0	567	1 ACFFA1	nicotinic acetylch
12	873	21.6	557	2 S12359	nicotinic acetylch
13	845	20.9	503	2 A53956	nicotinic acetylch
14	843.5	20.9	576	1 ACFFA2	nicotinic acetylch
15	841	20.8	521	1 ACFFNN	nicotinic acetylch
16	840	20.8	502	2 A37040	nicotinic acetylch
17	838	20.7	528	1 ACCH2N	nicotinic acetylch
18	828	20.5	511	2 A40110	nicotinic acetylch
19	827.5	20.5	456	1 ACCHAN	nicotinic acetylch
20	824	20.4	499	2 A24572	nicotinic acetylch
21	820.5	20.3	495	2 S60589	acetylcholine rece
22	820.5	20.3	512	2 B37014	nicotinic acetylch
23	817	20.2	494	2 T09289	nicotinic acetylch
24	806.5	19.9	500	2 S12899	nicotinic acetylch
25	805	19.8	498	2 G02421	nicotinic acetylch
26	802.5	19.8	457	1 ACHU41	nicotinic acetylch
27	801	19.8	457	1 ACBOA1	nicotinic acetylch
28	794.5	19.7	457	2 A28529	nicotinic acetylch
29	794	19.6	457	2 A24383	nicotinic acetylch

30	792.5	19.6	445	2	I49458	acetylcholine rece
31	789	19.5	457	2	S13872	nicotinic acetylch
32	789	19.5	470	2	A39218	nicotinic acetylch
33	787	19.5	491	1	ACCHNN	nicotinic acetylch
34	785	19.4	503	2	JH0174	nicotinic acetylch
35	783	19.4	461	2	I50548	acetylcholine rece
36	782	19.3	495	2	B35721	nicotinic acetylch
37	782	19.3	502	2	S10505	nicotinic acetylch
38	780	19.3	627	2	JC4021	nicotinic acetylch
39	779.5	19.3	559	2	E89134	protein F2566.4 [i
40	779.5	19.3	622	1	ACCHAN	nicotinic acetylch
41	779	19.3	461	1	ACRYA1	hypothetical prote
42	776	19.2	468	2	T24724	nicotinic acetylch
43	775.5	19.2	625	2	A26456	nicotinic acetylch
44	773.5	19.1	457	2	S08162	nicotinic acetylch
45	773	19.1	565	2	T23843	hypothetical prote

ALIGNMENTS

RESULT 1

A57175

nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Aug-1999
C;Accession: A57175
R;Orr-Urtreger, A.; Seidlin, M.F.; Baldini, A.; Beaudet, A.L.
Genomics 26, 399-402, 1995

A;Title: Cloning and mapping of the mouse alpha7-neuronal nicotinic acetylcholine rec
A;Reference number: A57175; MUID:95324936; PMID:7601470
A;Accession: A57175
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-502 <RR>

A;Cross-references: GB:L37663; NID:g790853; PID:AA2053.1; PID:g790854

C;Superfamily: acetylcholine receptor

C;Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprote

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr

F;231-254/Domain: transmembrane #status predicted <TR1>

F;262-280/Domain: transmembrane #status predicted <TR2>

F;296-317/Domain: transmembrane #status predicted <TR3>

F;470-488/Domain: transmembrane #status predicted <TR4>

F;46,90,133/Binding site: carboxylate (Asn) (covalent) #status predicted

F;365,413,427/Binding site: phosphate (Ser) (covalent) #status predicted

F;415/Binding site: phosphate (Thr) (covalent) #status predicted

F;442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 29.2%; Score 1182.5; DB 2; Length 502;

Best Local Similarity 45.8%; Pred. No. 5.1e-77;

Matches 239; Conservative 80; Mismatches 118; Indels 85; Gaps 10;

QY 297 IYINLSA---KVCAGYHEKRLHLLDPYNTLPRVNLNEDSPQLSFGTLQIIVDVE 353

DB 8 IWLAAALHVSLSQGEFQRRLKELVKNYNPLRPVANDSQPLTVYFSLQLQIMDVE 67

QY 354 KNOLLVTNVKLWMDNLRNTSDYGVKDLRIPPHRIWKPDVLMYNSADEGFCGTQY 413

DB 68 KNOVLTNTIWLQSWTDHYLQWNMSEYPGVKNVRFPGQIWKPDILLYNSADRFDFTFH 127

QY 414 TNYVVRNNGSCLYVPFGIFKSTCKIDITWPFDDQRCMKFGSWTYDGFOLDLQLODET 473

DB 128 TNLVNASGHCHQLPPGIFKSSCYIDVRWFFDVQCKLFGSKWSYGSWLDLQMQE--- 184

QY 474 GDTSYVNLNGEWELLGVPGKRNIEYNCCPEPIDITFAIIIRRTLYYFNFNLIIPCVLI 533

DB 185 ADISSYIPNGEWELMGIPGRNEKFEYECCKEYFDVTVTVMRRRTLYYGNLLIIPCVLI 244

QY 534 ASWALLGFTLPDPSGKSLSGVTLLSLTVFLNVAETMPATSDAVPL----- 581

DB 245 SALALLVFLLPADSGEKISIGITVLLSLTVFMLLVAEIMPATSDSVPLIAQYFASTMIIV 304

QY 582 -----WIRIVFLCWLPMILRMSRPG-----RPLILEPPTP 612
DB 305 GLSVVVTIVLYRHHDPDGKMPKWTIRIILNMCWFLMRKPGEDKVRACQHKPRR- 363
QY 613 CSDTSSERKHQILSDVELKERSKSLANVLIDDDFRHRCRPMPTGGTLPHPAFYRTV 672
DB 364 CS-----LASVELSAGAG-----PPTSNGNLYI--IGFRGL 392
QY 673 YGQ-----GDGSI--GPICSTRMPDAVTHHTCIKSTSEYELGLILKEIRFITDQLRKDDE 726
DB 393 EGMHCAPTDSGVVCGRLACSPTHDEHLMHGHTPSDGDPLAKILEEYRYIANRRCODE 452
QY 727 CNDIANDKFAAMVDRCLLIIFTMFAILATIAVLLSAPHII 768
DB 453 SEVICSEWKEACVYVDRCLLMAFSVFTIICITIGILMSAPNEV 494

RESULT 2
JN0113
A:Title: nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - chicken
N:Alternate names: alpha-bungarotoxin-binding protein alpha chain
C:Species: Gallus gallus (chicken)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 20-Aug-1999
C:Accession: JN0113; JN0172; S28018; B25738; S26566
R:Contourier, S.; Bertrand, D.; Matter, J.M.; Hernandez, M.C.; Bertrand, S.; Millar, N.; Neuron 5, 847-856, 1990
A:Title: A neuronal nicotinic acetylcholine receptor subunit (alpha 7) is developmentally essential for the formation of the neuromuscular junction in the chick embryo
A:Reference number: JN0113; MUID:91097796; PMID:1702646
A:Accession: JN0113
A:Molecule type: DNA
A:Residues: 1-502 <COU>
A:CROSS-references: GB:X68586; NID:9287756; PIDN:CAA48576.1; PID:g287757
A:Experimental source: white leghorn; brain
R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J. Neuron 5, 35-48, 1990
A:Title: Brain alpha-bungarotoxin binding protein cDNAs and MABS reveal subtypes of this protein
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0172
A:Molecule type: mRNA
A:Residues: 1-502 <SCH>
A:CROSS-references: EMBL:X52295; NID:g63077; PIDN:CAA36543.1; PID:g63078
A:Experimental source: brain
R:Matter-Sadziński, L.; Hernandez, M.C.; Roztocil, T.; Ballivet, M.; Matter, J.M. EMBO J. 11, 4529-4538, 1992
A:Title: Neuronal specificity of the alpha7 nicotinic acetylcholine receptor promoter determined by a 5' deletion analysis
A:Reference number: S28018; MUID:93049204; PMID:1425587
A:Accession: S28018
A:Molecule type: DNA
A:Residues: 1-18 <MAS>
A:CROSS-references: EMBL:X68246; GB:S49751; NID:g65319; PIDN:CAA48317.1; PID:g65320
A:Experimental source: white leghorn; erythrocyte
R:Conti-Tronconi, B.M.; Dunn, S.M.J.; Barnard, E.A.; Dolly, J.O.; Lai, F.A.; Ray, N.; Proc. Natl. Acad. Sci. U.S.A. 82, 5208-5212, 1985
A:Title: Brain and muscle nicotinic acetylcholine receptors are different but homologous
A:Reference number: A94055; MUID:85270494; PMID:3860855
A:Accession: B25738
A:Molecule type: protein
A:Residues: 24-25, 'ET', 28-41, 'X', 43-45, 'X', 47 <CON>
A:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is localized to the neuromuscular junction
C:Genetics:
A:Introns: 19/1; 65/3; 80/3; 117/2; 144/1; 200/1; 265/1; 294/1; 330/3
C:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; ion channel; neurotransmitter receptor; phosphoprotein; F.1-23/Domain: signal sequence #status predicted <SIG>
F.24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status predicted <TR1>
F.231-254/Domain: transmembrane #status predicted <TR2>
F.262-280/Domain: transmembrane #status predicted <TR3>
F.296-317/Domain: transmembrane #status predicted <TR4>
F.470-488/Domain: transmembrane #status predicted <TR5>
F.46-90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.365,367,413,427,465/Binding site: phosphate (Ser) (covalent) #status predicted
F.415/Binding site: phosphate (Thr) (covalent) #status predicted
F.442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 29.2%; Score 1179.5; DB 2; Length 502;
Best Local Similarity 45.7%; Pred. No. 8.3e-77;
Matches 237; Conservative 80; Mismatches 127; Indels 75; Gaps 9;
QY 295 LLIYLNLSA---KVCAGYHEKRLHLLDDPNTLERPVNLNESDPLQLSFGTLMOIIDV 351
DB 6 LMLLAAAGLVRESLOGEFQKLYKELLKNYLERPVANDSQPLTVFTTISLMOIMDV 65
QY 352 DEKNOLLVTNWLKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPDVLMYNSADEGFGDT 411
DB 66 DEKNQVLTNTWLQWYTDHYLOWNVSEYGPVKVNFDPDGLIWKPDILLYNSADERFDT 125
QY 412 YOTNVVRNNGSCLYVPGIFKSTCKIDITWFFPDQCEMKFGSWTYDGFOLDLQDDE 471
DB 126 FHTNVLVNSSGHCQYLPPIGIFKSSCYIDVRWFFDVQCNLFKGSWTYGGWSDLQMQE- 184
QY 472 TGGDISSVVLNGEWELLGVPGKRNIEIYNCCEPEYIDITFAIIIRRTLYYFNLIPCV 531
DB 185 --ADISGYISNGEWDLVGIPGKRTSEFYECCKEYPDITFTVTMRRRTLYYGLNLLIPCV 242
QY 532 LIASMAILGFTLPDPDSGEKLSLGVITLLSLTVFLNVAETMPATSDAVPL----- 581
DB 243 LISALALLVFLPADSGEKISIGIIVLLSLTVFLNVAEIMPATSDSPLIAQYFATMI 302
QY 582 -----WIRIVFLCWLPMILRMSRPGRLIILEFTTPCS 614
DB 303 IVGLSVVVTIVLYRHHDPDGKMPKWTIRIILNMCWFLMRKPG-----EDKVRPAC 357
QY 615 DTSSERKHQILSDVELKERSKSL--ANVLIDDDDFRH-----NCRPMPTGGTLPHPAFY 669
DB 358 QHKQRRCSS--LSSMEMMVTVSQOCSNGNMLYF--GFRGLDGVHCTFTTDSGVI----- 406
QY 670 RTVYGGDDSGISGPIGTSTMPDAVTHHTCIKSTSEYELGLILKEIRFITDQLRKDDECD 729
DB 407 -----CGRMTCSTEEENLHSGHSEGGDPLAKILEEYRYIANRFDQDEBA 455
QY 730 IANDWKFAAMVDRCLLIIFTMFAILATIAVLLSAPHII 768
DB 456 ICNEWKFAASVDRCLLMAFSVFTIICITIGILMSAPNEV 494

RESULT 3
T01378
A:Title: nicotinic receptor alpha 7 chain - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 21-Jul-2000
C:Accession: T01378
R:Sequela, P.; Wadiche, J.; Dineley-Miller, K.; Dani, J.A.; Patrick, J.W. J. Neurosci. 13, 596-604, 1993
A:Title: Molecular cloning, functional properties, and distribution of rat brain alpha 7 nicotinic receptor cDNA
A:Reference number: 214310; MUID:93147931; PMID:7678857
A:Accession: T01378
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <SEG>
A:CROSS-references: EMBL:S53987; NID:g264770; PIDN:AAB25224.2; PID:g5705903
A:Experimental source: brain
C:Superfamily: acetylcholine receptor

Query Match 29.0%; Score 1173.5; DB 2; Length 502;
Best Local Similarity 45.6%; Pred. No. 2.2e-76;
Matches 238; Conservative 80; Mismatches 119; Indels 85; Gaps 10;
QY 297 IYLNLSA---KVCAGYHEKRLHLLDDPNTLERPVNLNESDPLQLSFGTLMOIIDVDE 353
DB 8 IWLALAAALLHVSLOGEFQRLYKELVKNYLERPVANDSQPLTVFTSLSLQIMDVDE 67
QY 354 KQQLVLTNWLKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPDVLMYNSADEGFGTYQ 413
DB 68 KQVLTNTNWLQWYTDHYLOWNVSEYGPVKVNFDPDGLIWKPDILLYNSADERFDT 127
QY 414 TNVVRNNGSCLYVPGIFKSTCKIDITWFFPDQCEMKFGSWTYDGFOLDLQDDETG 473

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128 TNVLNASHGCOYLPGIEKSSCYIDVRWPFVQCKLKFSGWSYGGWSDLQMOE---184
QY 474 GDTSYVNGEWELGVLGPGKRNIEYNCCPEYIDITFAIIIRRTLYEFNLIICVLI 533
Db 185 ADISSYIPNGEWMOLGIPGARNKEFTECCKEPYPDVVTYIMRRRTLYGLNLIICVLI 244
QY 534 ASMALGFTLPDPSGKSLGVTLLSLTVFLNVAETMPATSDAVPL-----581
Db 245 SALALLVFLLPADSGEKISLGTIVLLSLTVFLMLVAEIMPATSDSVPLIAQYFASMTIIV 304
QY 582 -----WIRIVFLCWLWILRMSRPG-----RPLILEPPTTP 612
Db 305 GLSVVTVIVLRYHHDDPGKMPKWTRIILLNWCAMFLRMKPGEDKVRPACOHKPRR- 363
QY 613 CSDTSERKHQILSDVELKERSKSLLANVLDIDDDFRHNCRPMTPGGTLPHPNPAFRTV 672
Db 364 CS-----LASVELSAGAG-----PPTSGNLLY-IGFRGL 392
QY 673 YGQ-----GDDGSI-IGPISTRMPDAVTHHTCKSTSEYELGILKEIRITDOLRKDDE 726
Db 393 EGMHCAPTDPGSGVYVGRACSPTHDEHLMHGAHPSDGDPDLAKILEVRYIANRRCODE 452
QY 727 CNDIANDWKFAAMVVDRLCLIIITMFAILLATIAVLLSAPHII 768
Db 453 SEVICSEWKPACVDPDLCLMAFSVFTIICIGILMSAPNFV 494

RESULT 4
JH0173
alpha-bungarotoxin-binding protein alpha-2 chain precursor - chicken
C:Species: Gallus gallus (chicken)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Aug-1999
C:Accession: JH0173
R:Schoepfer, R.; Conroy, W.G.; Whiting, P.; Gore, M.; Lindstrom, J.
Neuron 5, 35-48, 1990
A>Title: Brain alpha-bungarotoxin binding protein cDNAs and Mabs reveal subtypes of this
A:Reference number: JH0172; MUID:90315158; PMID:2369519
A:Accession: JH0173
A:Molecule type: mRNA
A:Residues: 1-511 <SCH>
A:Cross-references: GB:X52296; NID:963081; PIDN:CAA36544.1; PID:963082
A:Experimental source: brain
A>Note: this sequence is similar to acetylcholine receptor alpha chains
C:Comment: Alpha-bungarotoxin binding proteins are localized to extrasynaptic pseudodend
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-510/Product: alpha-bungarotoxin binding protein alpha-2 chain #status predicted <AE
F:239-262/Domain: transmembrane #status predicted <TM1>
F:270-288/Domain: transmembrane #status predicted <TM2>
F:304-323/Domain: transmembrane #status predicted <TM3>
F:479-496/Domain: transmembrane #status predicted <TM4>
F:54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 28.9%; Score 1168; DB 2; Length 511;
Best Local Similarity 44.28; Pred. No. 5.7e-76;
Matches 238; Conservative 83; Mismatches 117; Indels 100; Gaps 12;

QY 285 NGLNKHSWIFLLYLNLSAKVCLAGYHEKRLLDLLDPYNTLPRPVNESDPLQSLGLT 344
Db 12 SGGLCLWASLFLSFF-----KVSQGESQRRLYDLRLNRLRPERVNMDSQPIVVELQLS 66
QY 345 LMQIIDVDENKQLLVTVNWLKLEWMDNLRWNTSDGVGVKDLRLTPHRIKWPDLVYNISA 404
Db 67 LLQIIDVDENKQVLITNANLQMTWVDIYLSWDQYEPGVONLRFPDSQIWPDLILYNISA 126
QY 405 DEGFDTGYQTNNVVRNNGSLYPPGIFKSTCKIDITWFFDDQRCMKFGSWTYDGFQL 464
Db 127 DERFDAFTHTNVLNYSQCOYIPPGILKSTCTVIDWRWPFVQKDLKFGSWTHSGWLI 186
QY 465 DLQLODTGGDISYVLNGEWELGVLGPGKRNIEYNCCPEYIDITFAIIIRRTLYYFF 524

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187 DLQMLE---ADISNYISNGEWDLVGVPGKRNIEYECCKEPYPDVVTYIMRRRTLYYGL 243
QY 525 NLIIPCVLIASMALLGFTLPDPSGKSLGVTLLSLTVFLNVAETMPATSDAVPL---581
Db 244 NLIIPCVLISGLALLVFLLPADSGEKISLGTIVLLSLTVFLMLVAEIMPATSDSVPLIAQ 303
QY 582 -----WIRIVFLCWLWILRMSRPG-----RPL 604
Db 304 YFASIMVIVGLSVVTVIVLQFHHDPQAGKMPWRVIRVILLNWCAMFLRMKPGENIKPL 363
QY 605 ILEFPTPCSDTSERKHQILSDVELKERSKSLLANVLDIDDDFRHNCRPMTPGGTLPHP 664
Db 364 SCAY-----SYRHHPSLKNTEM-----NVL-----PG-----H 387
QY 665 NPAFYRTVYG-----QGDD---GSIQIGSTRMPDAVTHHTCKIS---STEYELGLI 710
Db 388 QPSNGNMIYSHYTMENPCCQPNNDLGSKSKITCPLSED---NEHVOKKALMDTIPVIVKI 445
QY 711 LKIRFITDOLRKDDKDECDNDIANDWKFAAMVVDRLCLIIITMFAILLATIAVLLSAPHII 768
Db 446 LEEVQFIAMFRFRQDEGEIECESEKFAAAVIDRLCLVAFTLFAICTFTILMSAPNFI 503

RESULT 5
ACHUA7
nicotinic acetylcholine receptor alpha-7 chain precursor, neuronal - human
N:Alternate names: cholinergic nicotinate receptor alpha-7 chain
C:Species: Homo sapiens (man)
C>Date: 12-Aug-1996 #sequence_revision 31-Jan-1997 #text_change 22-Jun-1999
C:Accession: I37185; A54194; S60309
R:Peng, X.; Katz, M.; Gerzanich, V.; Anand, R.; Lindstrom, J.
Mol. Pharmacol. 45, 546-554, 1994
A>Title: Human alpha 7 acetylcholine receptor: cloning of the alpha 7 subunit from th
omers expressed in Xenopus oocytes.
A:Reference number: I37185; MUID:94195283; PMID:8145738
A:Accession: I37185
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <PEN>
A:Cross-references: EMBL:X70297; NID:9496606; PIDN:CAA49778.1; PID:9496607
A:Experimental source: brain neuroblastoma cell line SHSY-5Y
R:Chini, B.; Raimond, E.; Elgoyhen, A.B.; Moralli, D.; Balzarotti, M.; Heinemann, S.
Genomics 19, 379-381, 1994
A>Title: Molecular cloning and chromosomal localization of the human alpha-7-nicotini
A:Reference number: A54194; MUID:94245214; PMID:8188270
A:Accession: A54194
A:Molecule type: mRNA
A:Residues: 24-363,'S',365-374,'A',376-408,'AWPAP',414-502 <CHI>
A:Cross-references: GB:223141; NID:9457736; PIDN:CAA80672.1; PID:9457737
A:Experimental source: retina
C:Comment: This acetylcholine receptor is blocked by alpha-bungarotoxin and is locali
C:Genetics:
A:Gene: GDB:CHRNA7
A:Cross-references: GDB:138751; OMIM:118511
A:Map position: 15q14-15q14
A>Note: defects in this gene have been associated with mental retardation and schizop
C:Complex: the functional receptor molecule is a heteropentamer with two alpha chains
C:Superfamily: acetylcholine receptor
C:Keywords: brain; glycoprotein; heteropentamer; ion channel; neurotransmitter recept
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-502/Product: nicotinic acetylcholine receptor alpha-7 chain, neuronal #status pr
F:231-254/Domain: transmembrane #status predicted <TR1>
F:262-280/Domain: transmembrane #status predicted <TR2>
F:296-317/Domain: transmembrane #status predicted <TR3>
F:470-488/Domain: transmembrane #status predicted <TR4>
F:46,90,133/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:150-164/Diulfide bonds: #status predicted
F:365,413/Binding site: phosphate (Ser) (covalent) #status predicted
F:415/Binding site: phosphate (Thr) (covalent) #status predicted
F:442/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 28.7%; Score 1160.5; DB 1; Length 502;
Best Local Similarity 45.1%; Pred. No. 1.9e-75;

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[illegible]


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Db      362   TKPNRH-----SESLIRNIKNEHLSGRANSFDADCRLNQYIMTQSVS----- 404
Qy      667   AFYRTVYGDDG--SIGPIGSTRPMDAVTHHTCIKSTSEYELGLILKEIRFITDQLRKD 724
Db      405   -----NGLTSLGISPSTMISNGTTDVVSQQATLLIHLRIYHELKIYTKRMIEG 453
Qy      725   DECNDITANDWKFAAMVVORLCLIIPTFPAILATIAVLILLSAPHII 768
         : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      454   DKEEQACNNWKFKAAMVVDRLCYVFTEFIIVSTIGTFWSAPYL 497

RESULT 8
T25671
hypothetical protein D2092.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T25671
R:Gattung, S.: Maggi, L.
submitted to the EMBL Data Library, February 1997
A:Description: The sequence of C. elegans cosmid D2092.
A:Reference number: Z20067
A:Accession: T25671
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-461 <GAT>
A:Cross-references: EMBL:D88167; PIDN:AABA2223.1; GSPDB:GN000019; CESP:D2092.3
A:Experimental source: strain Bristol N2; clone D2092
C:Genetics:
A:Gene: CESP:D2092.3
A:Map position: 1
A:Introns: 36/1; 80/3; 119/2; 191/1; 243/1; 274/1; 303/1; 382/2
C:Superfamily: acetylcholine receptor

```

RESULT 9

T19622

hypothetical protein C31H5.3 - *Caenorhabditis elegans*

C: Species: *Caenorhabditis elegans*

C:\pcceres\cuencomodulos_cregans
C:\Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000

C: Access

R: Kershaw, J.

submitted to the EMBL Data Library. April 1997

A:Reference number: 219153

A,reference number: Z19133
A:Accession: T19622

A/ACCESSION: 115022
A/STATUS: preliminary. translated from GR/FMRL/DDRT

A-Molecule type: DNA

A; Molecule type: DNA
A: Residues: 1-560 WTTS

```
A;RESIDUES: I-360 <WIL>  
λ.CCCCCCCCCCCCCCC: EMDR .302778. PIDN.CAP07943 1. CCRDP.CN00010. CESP.C21HE 2
```

A; Cross-references: EMBL:Z93778; F

A; Experiment

C;Genetics:

A; Gene: CESP:C31H5

A;Map position: 1

A; Introns: 24/1; 70/3; 139/2; 270/1;

R;Hemby, C.

Submitted to the EMBL Data Library, March 1996

A:Reference number: Z19188

A:Accession: T19862

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-542 <WIL>

A:Cross-references: EMBL:Z70266; PIDN:CAA94206.1; GSPDB:GN00028; CESP:C40C9.2

A:Experimental source: clone C40C9

C:Genetics:

A:Gene: CESP:C40C9.2

A:Map position: X

A:Introns: 11/3; 69/3; 123/2; 173/3; 216/1; 248/1; 279/1; 314/1; 350/3; 430/1; 464/1; 49

C:Superfamily: acetylcholine receptor

Query Match 24.0%; Score 968.5; DB 2; Length 542;
Best Local Similarity 38.7%; Pred. No. 1.3e-61;
Matches 208; Conservative 79; Mismatches 144; Indels 107; Gaps 12;

QY 312 EKRLLHLLDPYNTLERPVNESDPLQSLFGLTLMQIIDVDEKNQLLVTVNWLKLEWDM 371

DB 30 EYRLADLRHNYDYPYRANASEPLVSVKIIYQQIILVDENKQVITLVAVIEYQWTDY 89

QY 372 NLRWNTSDYGVKDLRIP--PHRIWKPDVLMYNSADEGFDGTOTVNVVVRNNGSLVVP 429

DB 90 KLRWDPSEYGGIKDIRIPGNANALWKPDVLYNSADENFSTPYVNTVSYTGVDLVQVPP 149

QY 430 GIFKSTCKIDITWPFDDQRCMKFGSWTYDGFQDLQLQ-----DETGDDISSYVLN 482

DB 150 GILKLSCKIDITYPPDDQICHLKFGSWTYSNGFIDLRLNGPEGKNISDEGIDVOYVQN 209

QY 483 GEWELLVGPKRNEIYNCCPEYIDITFALIRRRITLYFFNLIIPCVLIASMALLGFT 542

DB 210 GENWLLAVPARHETNIF--EQYPSLFYLIQIRRTYILGLNLIIPSFLISLMTVLGFT 267

QY 543 LPDPSGEKLSGVITILLSVFLNMVAETMPATSDAVPL----- 581

DB 268 LPDAGEKIYLEITILLSVGFLLSNVADMTPTSEAVPLGLIIFSGAFSCCMVLYVAS 327

QY 582 -----WIRIVLCWLPILMRSPGRPLILEFTTPCSDTSSE 619

DB 328 VVFTVLNLNHRKPETHMSPEFLRELLIWLPLMLRRPGKTF-----NCTHLKAE 381

QY 620 RKHQILSDVELKE-----RSSKSLANV-----LDIDDDF--RHN-CRPM 656

DB 382 KAEKAKQSGIKNGVGKPTDSDVHPSEGLSLMKNIKLRQQTIDFYEFEVQHNLMPV 441

QY 657 TPGGTLPHNPAFYRTVYGGDGSIGPIGSTRMPDAVTHHTCIKSSTEY-----ELGLI 710

DB 442 APSEMTPE-----RVTY-----SKVMAESYVEDVWTELNKYMKACLELKN 483

QY 711 LKEIRFTDQLRKDDKDENDANDWKFAAMVVDRLCLIIFTWFAILATIAVLLSAPHII 768

DB 484 SSQTRAMRKMEEDERDEQAANDWKFAAMVVDRCCLITFSVFIVWTCGIMFSSPHLI 541

RESULT 11

ACFAI

nicotinic acetylcholine receptor alpha-1 chain precursor - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jun-2002

C:Accession: S00381; A38801

R;Bossy, B.; Ballivet, M.; Spierer, P.

EMBO J. 7, 611-618, 1988

A:Title: Conservation of neural nicotinic acetylcholine receptors from *Drosophila* to ver

A:Reference number: S00381; MUID:88283626; PMID:2840281

A:Accession: S00381

A:Molecule type: DNA

A:Residues: 1-567 <BOS>

A:Cross-references: GB:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576

A:Accession: A38801

A:Molecule type: mRNA

A:Residues: 1-567 <B02>

A:Cross-references: EMBL:X07194; NID:g7575; PIDN:CAA30172.1; PID:g7576

A:Note: 538-Tyr was also found

C:Genetics:

A:Gene: FlyBase:ncr-alpha-96Aa

A:Cross-references: FlyBase:FBgn0000036

A:Map position: 3R 96A

A:Introns: 64/3; 79/3; 116/2; 176/3; 330/2; 401/1; 499/3

C:Superfamily: acetylcholine receptor

C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-567/Product: nicotinic acetylcholine receptor alpha-like chain #status predicted

F:22-240/Domain: extracellular #status predicted <EXT>

F:240-264/Domain: transmembrane #status predicted <TM1>

F:272-290/Domain: transmembrane #status predicted <TM2>

F:306-325/Domain: transmembrane #status predicted <TM3>

F:326-513/Domain: intracellular #status predicted <INT>

F:514-532/Domain: transmembrane #status predicted <TM4>

F:514-533/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:149-163,222-223/Disulfide bonds: #status predicted

Query Match 22.0%; Score 889; DB 1; Length 567;

Best Local Similarity 35.2%; Pred. No. 6.7e-56;

Matches 196; Conservative 91; Mismatches 168; Indels 102; Gaps 10;

QY 291 SWIFLLIYLNLK-AKVCAGYHEKRLHLLDPYNTLERPVNESDPLQSLFGLTLMQII 349

DB 3 SVLFAAVFIALHFTATGGLAMPDAKRLYDLDLSNLRIRPVGNNSDLTKVMGLRSLI 62

QY 350 DVEKKNOLLTVNWLKLEWDMNLRWNTSDYGVKDLRIPPHRIWKPDVLMYNSADEGFD 409

DB 63 DVNLKNOIMTWVVEQENNDYKLNWPDYGGVDTLHVPSEHWHHPDILVLYNNADNYE 122

QY 410 GTYQTNVVVRNNGSLVPPGIFKSTCKIDITWPFDDQRCMKFGSWTYDGFQDL--- 466

DB 123 VTIMTKAILHHTGKVVWKPPAIYKSFCEIDVEYFPFDEQTCFMKFGSWTYDGYMVDLRLH 182

QY 467 -QLQD-----ETGGDISYVLNGEWELLVGPKRNEIYNCCPEYIDITFAIIIRRTLY 521

DB 183 KQTADSDNIEVGIDLDQYIISVEMDIMRVPVAVRNEKEYSCCEPYLDIVNLTLRRRTLF 242

QY 522 YFNLIIPCVLIASMALLGFTLPDPSGEKLSGVITILLSVFLNMVAETMPATSDAVPL 581

DB 243 YTVNLIIPCVGISFLSVFLVPLSDSGEKISLCISILLSLTVFPFLAEIIPPTSLVPL 302

QY 582 -----WIRIVLCWLPILMRSPGRPL 604

DB 303 LGKYLFTMLVTLVVVTVIAVLNVNFRSPVTHRMAMPVQVRLFIQLPKLCIERPKK-- 360

QY 605 ILEFPTTPCSDTSERKHOILSDV-ELKERSKSLANVLDIDDDFRHNCRPMTPPGTLP 663

DB 361 -----EPEEDQPPEVLTVDYHLLP-----DVKFVYVDSKRFSGDYGIP 400

QY 664 HNPAYR-----TVYQGSD-----GSIGPIGSTRMPDAVTH 695

DB 401 ALPASHRFDLAAAGGISAHCFABEPLPSSLPFGADDDLFSPSLNGDISGCCPAAAAA 460

QY 696 HTCIKST-----EYELGLILKEIRFTDQLRKDDKDENDANDWKFAAMVVDRLCLIFT 750

DB 461 AAADLSPTFEKPYAREMEKTIERSFTIAHQHVKNDKFESEEDWKYVAVMLDRMFLWIFA 520

QY 751 MFALATIAVLLSAPHI 767

DB 521 IACVVGTAIIILQAPSL 537

RESULT 12

S12359

nicotinic acetylcholine receptor alpha-L1 chain precursor - desert locust

C:Species: *Schistocerca gregaria* (desert locust)

C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999

C:Accession: S12359

R;Marshall, J.; Buckingham, S.D.; Shingai, R.; Lunt, G.G.; Goosey, M.W.; Darlison, M.

EMBO J. 9, 4391-4398, 1990

A;Title: Sequence and functional expression of a single alpha subunit of an insect nicotinic acetylcholine receptor
A;Reference number: S12359; MUID:91092263; PMID:1702381
A;Accession: S12359
A;Molecule type: mRNA
A;Residues: 1-557 <MAR>
A;Cross-references: EMBL:X55439; NID:g10133; PIDN:CAA39081.1; PID:g10134
C;Superfamily: acetylcholine receptor
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-557/Product: nicotinic acetylcholine receptor alpha-L1 chain #status predicted <MAT>
F;245-266/Domain: transmembrane #status predicted <TM1>
F;274-295/Domain: transmembrane #status predicted <TM2>
F;308-329/Domain: transmembrane #status predicted <TM3>
F;501-523/Domain: transmembrane #status predicted <TM4>
F;47,235/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.6%; Score 873; DB 2; Length 557;
Best Local Similarity 36.8%; Pred. No. 9.2e-55;
Matches 197; Conservative 90; Mismatches 174; Indels 74; Gaps 8;
QY 293 IFLLIYNLSAKVCLAGYHEKRLHLLDPYNTLRLPVLNESDPLQLSFGTLTLMQIIDVD 352
Db 8 MLLLLLLLLLHPAAAPDAKRLYDLLSNYRLRPVSNNTDTVLKGLRLSLQIDLN 67
QY 353 EKQOLLVTNWLKLEWDMNLRNWTSDYGVKDLRIPPHRIKPDVLMYNSADEGDTY 412
Db 68 LKQILLTNNWLEHEWQDKFRDPAEYGGVTELYPSEHILPDIVLYNADGEYVTT 127
QY 413 QTNVVRNNGSLVYPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFQDL----QL 468
Db 128 MTKAVLHHTGKVVTTPAIFKSCSIDVRYFPDQOTCFMKFGSWTYDGDQIDKHINQ 187
QY 469 QDE-----TGDDISSYVLNGEWELLVPGKREIYVNCPEPYIDITFAIIRRTLYYFF 524
Db 188 YDNKVKVGDILREYPSVEMDILGVAERHEKYCCAPYDPIDFENITLRKTFYTV 247
QY 525 NLIIPCVLIASMLLFTLPDPSGEKLSGLVITLLSLTVPLNVAETMPATSDAVPL--- 581
Db 248 NLIIPCVGISYLVFLPADSGEKIALCISILLSTQMPFLITSEIIPSTSLALPLGK 307
QY 582 -----WTRIVFLCWLPLTMRSPGRPLILE 607
Db 308 YLFTWVLGSLVITIMLVNHYRKPSTHKMAPVWKVFIRLPKLLLMRVEQLL--- 364
QY 608 FPTTPCSDTSERKHQILSDVELKERSKSLA-----NVLIDDDFRHN----- 652
Db 365 -----ADLASKRLRLRAHNSKLSAAAAAARAAASSPDSLRLHHHLHQHQHHL 418
QY 653 --CRPMTPGTLPHPNPAFYRTVYGGDDGSGIGPSTMPDPVTHHTFCIKSSTEYELGLI 710
Db 419 QLHHLQRPQGCNGLHSATNR--FG-GSAGAFGLPSVVGDLGSLSDVATRKYPFELEKA 475
QY 711 LKEIRFTDOLRKDDCNDIANDKFAAMVVDRLCLIFTMFAILLATIAVLLSAP 765
Db 476 IHNVLFIQNHQKQDEDAEDQWGFVAMVDRLFLWIFTIASIVGTFAILCEAP 530

RESULT 13
A53956
nicotinic acetylcholine receptor alpha-3 chain precursor, neuronal - human
C;Species: Homo sapiens (man)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 20-Aug-1999
C;Accession: A53956; S21338
R;Mihovilovic, M.; Roses, A.D.
Exp. Neurol. 111, 175-180, 1991
A;Title: Expression of mRNAs in human thymus coding for the alpha3 subunit of a neuronal
A;Reference number: A53956; MUID:91114756; PMID:1989896
A;Accession: A53956
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-503 <MTH>
A;Cross-references: GB:M37981; NID:g189252; PIDN:AAAS9942.1; PID:g189253
R;Anand, R.; Lindstrom, J.

submitted to the EMBL Data Library, June 1990
A;Description: Nucleotide sequence of the mature human nicotinic acetylcholine receptor
A;Reference number: S21338
A;Accession: S21338
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 30-503 <ANA>
A;Cross-references: EMBL:X53559; NID:g34985; PIDN:CAA37625.1; PID:g34986
C;Genetics:

A;Gene: GDB:CHRNA3
A;Cross-references: GDB:125219; OMIM:118503
A;Map position: 15q24-15q24
C;Superfamily: acetylcholine receptor
C;Keywords: neurotransmitter receptor

Query Match 20.9%; Score 845; DB 2; Length 503;
Best Local Similarity 35.2%; Pred. No. 8.2e-53;
Matches 178; Conservative 97; Mismatches 166; Indels 64; Gaps 6;
QY 295 LLIYLNLSAKVCLAGYHEKRLHLLDPYNTLRLPVLNESDPLQLSFGTLTLMQIIDVDEK 354
Db 17 LLLLLSL-LPVARASEAEHRLFERLPEDYNEIIRPVANVSDPVIHFEVMSQSLVKVDE 75
QY 355 NQLLVTVNWLKLEWDMNLRNWTSDYGVKDLRIPPHRIKPDVLMYNSADEGDTGYOT 414
Db 76 NQIMETNLWLKQIWNQYKLNWSPDYGAEFMVRPAQKIWKPDIVLYNNAVGDFQVDDKT 135
QY 415 NVVVRNNGSLVYPGIFKSTCKIDITWFPDDQRCMKFGSWTYDGFQDLQLODDETG 474
Db 136 KALKYTGVTWTPAIFKSSCKIDVTFYFPDQOTCFMKFGSWTYDGDQIDKHINQ 194
QY 475 DISSYVLNGEWELLVPGKREIYVNCPEPYIDITFAIIRRTLYYFFNLIPCVLIA 534
Db 195 NLADYEWESGEWATIKAPGYKHKIKYCCREIYDITVSLVIRLPFLTYTNLIIPCLIS 254
QY 535 SMALLGFTLPDPSGEKLSGLVITLLSLTVPLNVAETMPATSDAVPL----- 581
Db 255 FLTVLFLYLPDSCGEKVTLCISVLLSLTVFELLITIPSTSLVPLIGLYLLTFMTFVT 314
QY 582 -----WTRIVFLCWLPLTMRSPGRPLILEFPTTPCSDTS 617
Db 315 LSIVITVFLNVHYRTPHTMPSWKVTFVLLLPV-----FMTRPTSNEG 362
QY 618 SERKHQILSDVELKERSKSLANLVIDDDFRHNCRPMTPGTLPHNPAFYRTVYGGDD 677
Db 363 NAQKPRPLYGAELSNLNCFSRAES-----KGCKEGYPCODGCMGCHHRRIKISNF 413
QY 678 DGSIGIGSTMPDPVTHHTFCIKSSTEYELGLILKEIRFTDQLRKDDCNDIANDKFA 737
Db 414 SANLTRSSSESVDVLS-----LSALSPEIKAEIQSVKYIAENKKAQNEAKETODDKYV 469
QY 738 AMVVDRLCLIFTMFAILLATIAVLL 762
Db 470 AMVIDRFLWVTLVLCILTAGLFL 494

RESULT 14
ACFFA2
nicotinic acetylcholine receptor alpha-2 chain precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jun-2002
C;Accession: S11679; S10306; S11084
R;Sawruk, E.; Schloss, P.; Betz, H.; Schmitt, B.
EMBO J. 9, 2671-2677, 1990
A;Title: Heterogeneity of Drosophila nicotinic acetylcholine receptors: SAD, a novel
A;Reference number: S11679; MUID:90360975; PMID:1697262
A;Accession: S11679
A;Molecule type: mRNA
A;Residues: 1-576 <SAW>
A;Cross-references: EMBL:X53583; NID:g8532; PIDN:CAA37652.1; PID:g8533
A;Note: 232-ile was also found
R;Baumann, A.; Jonas, P.; Gundelfinger, E.D.
Nucleic Acids Res. 18, 3640, 1990

A:Title: Sequence of D-alpha-2, a novel alpha-like subunit of Drosophila nicotinic acetylcholine receptor
A:Reference number: S10306; MUID:90301489; PMID:2114015
A:Accession: S10306
A:Molecule type: mRNA
A:Residues: 1-576 <BAU>
A:Cross-references: EMBL:X52274; NID:g7802; PIDN:CAA36517.1; PID:g7803
R:Jonas, P.; Baumann, A.; Merz, B.; Gundelfinger, E.D.
FEBS Lett. 268, 1990
A:Title: Structure and developmental expression of the D-alpha-2 gene encoding a novel nicotinic acetylcholine receptor
A:Reference number: S11084; MUID:90353591; PMID:2117557
A:Accession: S11084
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 42-90, 'I', '92-576 <JON>
C:Genetics:
A:Gene: FlyBase:nACR-alpha-96Ab
A:Cross-references: FlyBase:FBgn0000039
A:Map position: 3R 96A
A:Introns: 84/3; 136/2; 196/3; 250/1; 445/2; 512/3
A:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membrane;
F:1-41/Domain: signal sequence #status predicted <SIG>
F:42-576/Product: nicotinic acetylcholine receptor alpha-2 chain #status predicted <WAT>
F:42-260/Domain: extracellular #status predicted <EXT>
F:261-287/Domain: transmembrane #status predicted <TM1>
F:293-311/Domain: transmembrane #status predicted <TM2>
F:327-348/Domain: transmembrane #status predicted <TM3>
F:349-526/Domain: intracellular #status predicted <INT>
F:527-545/Domain: transmembrane #status predicted <TM4>
F:65,254,570/Binding site: carbonylate (Asn) (covalent) #status predicted
F:169-183/Disulfide bonds: #status predicted

Query Match 20.9%; Score 843.5; DB 1; Length 576;
Best Local Similarity 34.4%; Pred. No. 1.3e-52;
Matches 193; Conservative 87; Mismatches 170; Indels 111; Gaps 11;

QY 290 HSW-----IFLLIYLNLSAKVCLAGYHEKRLHLLDPYNTLERPVNLNESPLOLSFGILT 344
DB 18 HIWRCKPLCLLLVLLLCETVOANPDARKLYDILLSNYNRLIRPVSNNTDTVLKGLR 77
QY 345 LMOIIDVDEKNOLLVTNWLKLEWDMNLRNWTSDYGVKDLRIPPHRIKVPDVLVYN 404
DB 78 LSOLDLNLKDOILTNWLEHWDHFKFDPSEYGVTELYVPSEHILPDLVLYNNA. 137
QY 405 DEGFDTGTQTNVVRNNGSCLYPPGIFKSTCKIDITWFFDDQRCCKMFGSWTYDGFQL 464
DB 138 DGEYVVTMTKAILHTYTKVWVTPPAIFKSSCEIDVRYFPDQDQCFCKMFGSWTYDGPQI 197
QY 465 DL-----QLQD-----ETGDDISSYVLNGEWELLYGVPGRNEIYNCCPEYDITFAIII 515
DB 198 DLKHISQRNDKDKVEIGIDREYYPSEVDILGVPAERHEKHYPCCAEYPDIPFNITL 257
QY 516 RRTLYYFNLIIPCVLIASMALGFTPPDQSGEKLGLVITLLSLTVFLANVAETMPAT 575
DB 258 RKTLFTYVNLIPCVGISYLSVLVFLPADSGEKALICISILLSQTMFFLISILIPST 317
QY 576 SDAPVL-----WIRYVFLCWLPWILRMS 598
DB 318 SLALPLKGLYLLFTMLLVGLSVITIIILNIHYRKPSTHKRWPWIRSFPIKRLPKLLMR 377
QY 599 RGRPLILEFTPTPCSDTSSEKHOILSDVELKE-----RSKSLANVLIDDDFRNC 653
DB 378 VP-----KDLRLDLANKINYGLKFSKTEKFGQAL-MDE----- 409
QY 654 RPTPGGTLPHNPAFYRTVYGOD-----DGSGTGPICS-----TRMPDA 692
DB 410 MQMNSGGSPSLRRMQGRVAGGCGNMHVTTATNRFSGLVGALCGGLSTLSGYNGLP 469
QY 693 VT-----HHTCIKSTSEYELGLILKEIRFTDQKDECDNDIANDKFAAMVDRCL 746
DB 470 LSGLDLSLSDVAARKKYPFELEKAIHNVWFIOQHMQRQDEFNADQDQGFVAMVDRFL 529
QY 747 IIFTFAIATAVLLSAPHI 767

DB 530 WLFMIASLVGTFTVLGEAPSL 550
RESULT 15
ACFFNN
C:Species: Drosophila melanogaster
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 22-Jun-1999
C:Accession: S03012; A38064; A26313; A28126; A38759
R:Savruk, E.; Hermans-Borgmeyer, I.; Betz, H.; Gundelfinger, E.D.
FEBS Lett. 235, 40-46, 1988
A:Title: Characterization of an invertebrate nicotinic acetylcholine receptor gene: t
A:Reference number: S03012; MUID:88296842; PMID:3136037
A:Accession: S03012
A:Molecule type: DNA
A:Residues: 1-521 <SAW>
A:Cross-references: EMBL:X07956; NID:g7602; PIDN:CAA30778.1; PID:g1065712
A:Accession: A38064
A:Molecule type: mRNA
R:Hermans-Borgmeyer, I.; Zopf, D.; Ryseck, R.P.; Hovemann, B.; Betz, H.; Gundelfinger
EMBO J. 5, 1503-1508, 1986
A:Title: Primary structure of a developmentally regulated nicotinic acetylcholine rec
A:Reference number: A26313
A:Molecule type: mRNA
A:Residues: 1-72, 'V', '74-521 <HER>
A:Cross-references: EMBL:X04016; NID:g7537; PIDN:CAA27641.1; PID:g7538
R:Wadsworth, S.C.; Rosenthal, L.S.; Kammermeyer, K.L.; Potter, M.B.; Nelson, D.J.
Mol. Cell. Biol. 8, 778-785, 1988
A:Title: Expression of a Drosophila melanogaster acetylcholine receptor-related gene
A:Reference number: A28126; MUID:88174720; PMID:2832736
A:Molecule type: mRNA
A:Residues: 1-521 <WAD>
A:Cross-references: EMBL:M20316
C:Genetics:
A:Gene: ard
A:Cross-references: FlyBase:FBgn0000038
A:Map position: 3L 64B/C
A:Introns: 22/1; 67/3; 119/2; 267/3; 467/3
C:Superfamily: acetylcholine receptor
C:Keywords: glycoprotein; ion channel; neurotransmitter receptor; postsynaptic membra
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-521/Product: nicotinic acetylcholine receptor nonalpha chain #status predicted <
F:25-236/Domain: extracellular #status predicted <EXT>
F:237-260/Domain: transmembrane #status predicted <TM1>
F:268-285/Domain: transmembrane #status predicted <TM2>
F:302-323/Domain: transmembrane #status predicted <TM3>
F:324-481/Domain: intracellular #status predicted <INT>
F:482-500/Domain: transmembrane #status predicted <TM4>
F:48/Binding site: carbonylate (Asn) (covalent) #status predicted
F:152-166/Disulfide bonds: #status predicted

Query Match 20.8%; Score 841; DB 1; Length 521;
Best Local Similarity 35.6%; Pred. No. 1.7e-52;
Matches 186; Conservative 95; Mismatches 172; Indels 70; Gaps 9;

QY 291 SWIFLLIYNLSAKVCLAGYHEKRLHLLDPYNTLERPVNLNESPLOLSFGILTMOIID 350
DB 7 SWLJCSILVLAFAVLSVASEDEERLVRLDFRGYNKLRIPVQNMOTKQVGRFGLAVQLIN 66
QY 351 VDEKNOLLVTNWLKLEWDMNLRNWTSDYGVKDLRIPPHRIKVPDVLVYN 410
DB 67 VNEKNQIMKSNVNLRLVWYDQLQWDEADYGGIGVLRPLPPDKVWKPDLVFNADGNVEY 126
QY 411 TYQTNVVRNNGSCLYPPGIFKSTCKIDITWFFDDQRCCKMFGSWTYDGFQLQL-Q 469
DB 127 RYKSNVLIYPRGEVLWVPPAIYQSSCTIDVTYFPDQDQTCIMKFGSWTFNGDQVSLALYN 186
QY 470 DETGDDISSYVLNGEWELLYGVPGRNEIYNCCPEP-YIDITFAIIRRTLYYFNLI 528

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Db 187 NKNFVLSYWKSGTWDIIIEVPAYLN-VYEGDSNHPTETDITFYIIIRKTLFYTVNLIL 245
QY 529 PCVLIASMAIIGFTLPDPSGKLSLGTILLSLTVFLNMVAETMPATS----- 576
Db 246 PTVLISFLCVLYFLPAEAGEKVTLGISILLSVVFLLVSKILPPTSLLVPLIAKYLLF 305
QY 577 -----DAVPLWIRIVFLCWLPMILRMSRGRPLILEFPTT 611
Db 306 TFIIMTVSILVTVIIINWNFRGPRTHRMMPYIRSFHYLPAFLPMKRPKTRLRMMEM 365
QY 612 PCSDTSSERKHQILSDVELKERSS-----KSLLANVLIDDDFRHNC---RPMTPGCTLPH 664
Db 366 PGMSMPAHPHPYSGPAELPKHISATGGKSKMEVMEISDLHHPNCKINRKVNSGEL-- 423
QY 665 NPAFYRTVYQGDGDSIGPIGSTRMPDAVTHHTCIKSSTEYELGLILKEIRFITDOLRKD 724
Db 424 -----GLGD---GCRRESSESDSILLSPEASKATE-----AVEFIAEHLRNE 462
QY 725 DECNDIANDKFAAMVVDRLCLIIETMFAILATIIVLLSAPHI 767
Db 463 DLYIQTREDWKYVAMVIDRLQLYIFFIVTTAGTVGILMDAPHI 505
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Job time : 30.7606 secs

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OM protein - protein search, using sw model

Run on: August 13, 2003, 15:14:30 ; Search time 67.5439 Seconds
(without alignments)
1809.483 Million cell updates/sec

Title: US-09-303-232-2

Perfect score: 4043

Sequence: 1 MKNAQLKTEVDDDELWLAV.....MFAILTAVLLSAPHIIVS 770

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4043	100.0	770	21	AA198014
2	1850	45.8	496	21	AA198115
3	1609	39.8	501	21	AA198216
4	1498.5	37.1	327	22	AB170382
5	1407.5	34.8	311	22	AB170383
6	1179.5	29.2	502	18	AA112368
7	1168	28.9	511	18	AA112369
8	1159.5	28.7	502	15	AA112370
9	1159.5	28.7	502	18	AA198025
					D. melanogaster ac
					H. virescens acety
					H. virescens acety
					Drosophila melanog
					Drosophila melanog
					Neuronal alpha-bun
					Neuronal alpha-bun
					Human neuronal nic
					Neuronal nicotinic

10	1159.5	28.7	502	21	AA198014
11	1159.5	28.7	502	22	AA198115
12	1159.5	28.7	502	22	AA198216
13	1159.5	28.7	502	23	AB170382
14	1159.5	28.7	502	23	AB170383
15	1159.5	28.6	502	19	AA198014
16	1159.5	28.5	502	22	AA198015
17	1159.5	28.4	502	22	AA198016
18	1159.5	28.3	502	22	AA198017
19	1159.5	28.3	502	22	AA198018
20	989	24.5	193	22	AA198019
21	972	24.0	554	22	AA198020
22	972	24.0	554	24	AB170382
23	922.5	22.8	470	22	AA198014
24	912	22.6	448	22	AA198018
25	848.5	21.0	529	15	AA198015
26	848.5	21.0	529	16	AA198016
27	848.5	21.0	529	18	AA198022
28	848.5	21.0	529	23	AB170382
29	848.5	21.0	529	23	AB170383
30	848.5	21.0	529	23	AB170384
31	847.5	21.0	772	22	AA198018
32	845	20.9	504	18	AA198022
33	843.5	20.9	576	22	AA198025
34	841	20.8	521	22	AA198026
35	834	20.6	631	23	AA198027
36	831.5	20.6	580	22	AA198028
37	829.5	20.5	479	22	AA198029
38	829.5	20.5	479	24	AB170382
39	826.5	20.4	552	22	AA198030
40	822.5	20.3	622	23	AA198031
41	822.5	20.3	622	23	AA198032
42	821.5	20.3	502	22	AA198033
43	815.5	20.2	519	22	AA198034
44	805	19.9	498	18	AA198035
45	805	19.9	498	23	AB170382

ALIGNMENTS

RESULT 1
AA198014
ID AA198014 standard; Protein; 770 AA.
XX
AC AA198014;
XX
DT 17-FEB-2000 (first entry)
XX
DE D. melanogaster, acetyl-choline receptor protein from clone Da7.
XX
DE Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
KW neurotransmission; plant protection agent; conductance; AChR.
XX
OS Drosophila melanogaster.
XX
PN DE19819829-A1.
XX
PD 11-NOV-1999.
XX
PF 04-MAY-1998; 98DE-1019829.
XX
PR 04-MAY-1998; 98DE-1019829.
XX
PA (FARB) BAYER AG.
XX
PI Adamczewski M, Oellers N, Schulte T;
XX
DR WPI; 2000-014207/02.
XX
DR N-PSDB; AAZ24475.
XX
PT New nucleic acid encoding a nicotinic acetylcholine receptor from insects, used to identify potential insecticides

Db 244 NLLIPCVLLISGLALLVLLPADSGEKISLGTIVLLSVFLLVAEIMPATSDSVPLIAQ 303
 Qy 582 -----WIRIVELCWLPWILMSRPG---RPL 604
 Db 304 YFASIMVIGLSVVTVLVLFQHHDPQAGKMPWRVRVILLNWCWFLMKKPGENIKPL 363
 Qy 605 ILEFPTPCSTSSRKHQILSDVELKERSKSLANVLDIDDDFRHNCRPMTPGGTLPH 664
 Db 364 SCKY-----SYPKHPSLKNTEM-----NVL-----PG-----H 387
 Qy 665 NPAFYRTYVG-----QGDD--GSIGPIGSTRMPDVAHTHTCIKS--STEYELGLI 710
 Db 388 QPSNGNMIYSYHTMENPCPONNDLGSKGITCPLSED--NEHVQKKALMDTIPVIVKI 445
 Qy 711 LKEIRFIQDLRKDECDIANDKFAAMVVDRLCLIIFTMFALITAVLLSAPHII 768
 Db 446 LEEVQFIAMRRKQDEGEICESEKFAAAVIDRCLVAFTLFAICTFTILMSAPNFI 503

RESULT 8

AAW44153
 ID AAW44153 standard; Protein; 502 AA.

XX AC AAW44153;

DT 14-MAY-1998 (first entry)

XX Human neuronal nicotinic acetylcholine receptor alpha-7 subunit.

XX Human; neuronal nicotinic acetylcholine receptor; alpha-7 subunit;
 KW brain tissue; screening; NACHR; antibody.

XX Homo sapiens.

FX Key Location/Qualifiers

FT Peptide 1..23

FT /label= signal

FT Domain 229..256

FT /label= TMD1

FT /note= "transmembrane domain"

FT Domain 262..284

FT /label= TMD2

FT /note= "transmembrane domain"

FT Domain 290..317

FT /label= TMD3

FT /note= "transmembrane domain"

FT Misc-difference 343

FT /note= "encoded by CTS"

FT Domain 462..487

FT /label= TMD4

FT /note= "transmembrane domain"

FT Domain 318..461

FT /label= cytoplasmic_loop

XX WO9420617-A2.

PN

XX 15-SEP-1994.

PD

XX 08-MAR-1994; 94WO-US02447.

XX 08-MAR-1993; 93US-0028031.

XX (SALK) SALK INST BIOTECHNOLOGY IND ASSOC.

PA (SIBI-) SIBIA NEUROSCIENCES INC.

XX Elliott KJ, Ellis SB, Harpold WM;

XX WPI; 1994-303024/37.

DR N-PSDB; AAV12197.

XX Human neuronal nicotinic acetylcholine receptor subunits and DNA -

PT also transformed cells useful for screening cpds. which modulate

PT activity of the receptor

PS Claim 7; Page 80-81; 99pp; English.

CC The present sequence represents a human neuronal nicotinic acetylcholine
 CC receptor (NACHR) subunit. The cells expressing the alpha and/or beta
 CC NACHR subunits may be used in a method of screening compounds to
 CC identify any which modulate the activity of human neuronal NACHR.
 CC Subunit specific antibodies may be used to monitor the distribution
 CC and expression density of various subunits in normal vs diseased brain
 CC tissues. Testing of single receptor subunits or specific receptor
 CC subunit combinations with a variety of potential agonists or antagonists
 CC provides information with respect to the function and activity of the
 CC individual subunits and should lead to the identification and design of
 CC compounds that are capable of very specific interaction with one or
 CC more receptor subtypes. The resulting drugs should exhibit fewer
 CC unwanted side effects than drugs identified e.g. screening with cells
 CC that express a variety of subtypes.

XX Sequence 502 AA;

Query Match 28.7%; Score 1159.5; DB 15; Length 502;

Best Local Similarity 45.1%; Pred. No. 1.4e-97;

Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;

Qy 297 IYLNLSAK---VCLAGYHEKRLLDLDPPYNTLPRVNLNESPQLSGLIMQIIVDE 353

Db 8 VWLALASLLHVSQGEFQRLKYLKYNPNLERPVANDSQPLTVYFSLSLQIMVDE 67

Qy 354 KNOLLVYNWLKLEWDMNLWNTSDYGVKDLRIPPHRIWKPVDVLMVNSADEGPDGTYQ 413

Db 68 KQVLTNTINILQMSNTDHYLQWNVSEYPGVATVRFPDQGIWKPDLILNSADERDAIFH 127

Qy 414 TNVVRNNGSLYVPPGIFKSTCKIDITWFFDQRCMKFGSWTYDGFOLDLQDDETG 473

Db 128 TNVLNNSGHCQYLPPIGIFKSSCYIDVWFFDVQHKLFSGWSYGGWSDLQWQE--- 184

Qy 474 GDISSYVLNGEWELLGVPGKNEIYNNCCPEYIDITFALIRRTLYFFNLIPCVLI 533

Db 185 ADISGYIPNGEWDLVGIFGRSERFYECCKEPPDVTFTVMRRRTLYYGLNLIPCVLI 244

Qy 534 ASMALGFTLPDSDGEKISLGVITLLSLTVFLNVAETMPATSDAVPL----- 581

Db 245 SALALLVFLPADSGEKISLGVITLLSLTVFLNVAETMPATSDVPLIAQYFASTMIIV 304

Qy 582 -----WIRIVELCWLPWILMSRPG-----RPLILEFFTP 612

Db 305 GLSVVTVIVLQYHHDDPDGKMPKATRVILLNWCWFLMKRPGEDKVRP-ACQHKORR 363

Qy 613 CSDTSSERKHQILSDVELKERSKSLANVLDIDDDFRH-----NCRPMTPGGTLPHNPAF 668

Db 364 CSLASVE-----MSAVAPPASNGNLLY-----IGFRGLDGVHCVP-TP----- 401

Qy 669 YRTVYGGDDGSGIGPIGSTRMPDVAHT-----HTCIKSSTEYELGLIKELIRFTDQURK 723

Db 402 -----DSGVV-----CGRMACSPTHDEHLHGQPPGDPDLAKILEEVRVYIANRPRC 449

Qy 724 DDECDIANDKFAAMVVDRLCLIIFTMFALITAVLLSAPHII 768

Db 450 QDESEAVCSEKFAACVVDRLCLMAFSVFTICTIGILMSAPNEV 494

RESULT 9

AAW09025

ID AAW09025 standard; Protein; 502 AA.

XX AC AAW09025;

XX 09-APR-1997 (first entry)

DT Neuronal nicotinic acetylcholine receptor alpha-7 subunit.

XX Neuronal nicotinic acetylcholine receptor; NACHR; neurotransmitter;

XX Neuronal nicotinic acetylcholine receptor; NACHR; neurotransmitter;

CC PRO polynucleotide and protein sequences given in the exemplification of
 XX the present invention.
 XX
 SQ Sequence 502 AA;

Query Match 28.7%; Score 1159.5; DB 21; Length 502;
 Best Local Similarity 45.1%; Pred. No. 1.4e-97;
 Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;

QY 297 IYLNLSAK---VCLAGYHEKRLHDLDPYNTLPRVNLNESDPLQLSFLGLTLMQIDVDE 353
 DB 8 VMLAALASLLHVSLOGEFQRLKLYELVKNYPLRPVANDSQPLTVYFSLSLQIMDVE 67

QY 354 KNOILLVTNWLKLEWDMNLRWNTSDYGGVKDLRIPPHRIWKPVDVMTNSADEGFDGYQ 413
 DB 68 KNOVLTNWLQMSWTDHVQWNVSEYPCVKTVPFPGQIKWPKDILLNSADERFDATEFH 127

QY 414 TNVVRNNGSLYPPGIFKSTCKIDITWFFDDQRCCKMFGSWTYDGFQDLQLODETG 473
 DB 128 TNVLNNSGHCQYLPFGIFKSSCYIDVRWFPDVQHCCLKFGWSYGGWSLDQMQE--- 184

QY 474 GDISSYVLNGEWELLGVPCKNEIYNGCPPEYIDITFAIIRRTLYFFNLIIPCVLI 533
 DB 185 ADISCIYINGEWDLVGICRSERYECKPEYDPVTVVWRTLYIYGLNLLIPCVLI 244

QY 534 ASMLLGTFLPDSGEKLSGLVITLLSLTVLNMVAETMPATSDAVPL----- 581
 DB 245 SALALLVLLPADSGEKISLGITVLLSTVFMVLLVAEIMPATSDSVPLIAQYFASTMIIV 304

QY 582 -----WIRVFLCWLPIILRMRPG-----RPLLEFPPTP 612
 DB 305 GLSVVVTVIVLYQHHPDGCKMPKWTIVILLNCWAFMRKRGEDKVRP-ACQHKQRR 363

QY 613 CSDTSSERKHQILSDVELKRSKSLANVLIDDDFRH---NCRPMTPGGTLPHPNPAF 668
 DB 364 CSLASVE-----MSAVAPPASGNLLY-----IGFRGLDGVHCV-TP----- 401

QY 669 YRTVYGGQDGSIGPIGSTRMPDAVTH-----HTCIKSSTYEGLILKEIRFTDQURK 723
 DB 402 -----DSGVV-----CGRMACSPTHDEHLHGQPPGDPDLAKILEEVRYIANRRC 449

QY 724 DDECNDIANDKFAAMVVDRLCLIFTFAILATIATVLLSAPHII 768
 DB 450 QDESAVCEWKAACVVDRLCLMAFSVFTICTIGILMSAPNFV 494

RESULT 11
 AAB82690
 ID AAB82690 standard; Protein; 502 AA.
 XX
 AC AAB82690;
 XX
 DT 15-OCT-2001 (first entry)
 XX
 DE Nicotinic acetylcholine receptor alpha7.
 XX
 KW Nicotinic acetylcholine receptor; nAChR; human;
 KW ligand-binding protein; AChBP; mollusc;
 KW ligand-binding protein; ligand-gated ion channel; crystal;
 KW drug design; protein co-ordinate data; schizophrenia;
 KW Alzheimer's disease; nicotine addiction; Tourette's syndrome;
 KW therapy; nootropic; neuroprotective.
 XX
 OS Homo sapiens.
 XX
 FH Location/Qualifiers
 FT 108..115
 FT /note= "conserved ligand-binding region, residues
 Trp108 and Tyr115 are essential"
 FT 171..173
 FT /note= "conserved ligand-binding region, residues
 Trp171 and Tyr173 are essential"
 FT 210..217

/note= "conserved ligand-binding region, residues
 Tyr210, Cys212, Cys213 and Tyr217 are
 essential"

WO200158951-A2.
 XX
 XX 16-AUG-2001.
 PD
 XX
 PF 09-FEB-2001; 2001WO-EP01457.
 XX
 XX 10-FEB-2000; 2000EP-0200443.
 PR 31-OCT-2000; 2000EP-0203810.
 XX
 XX (TEWE-) STICHTING TECH WETENSCHAPPEN.
 PA Smit AB, Sixma TK;
 PI
 XX WPI; 2001-497071/54.
 DR
 XX Water-soluble ligand-binding proteins derived from molluscs and analogues
 of ligand-gated ion channels, useful in drug screening assay, where the
 drugs identified can be used in the treatment of Alzheimer's disease or
 schizophrenia
 XX
 PS Disclosure; Page 252-254; 260pp; English.
 XX
 CC The present sequence is that of the alpha subunit of human
 CC nicotinic acetylcholine receptor (nAChR). The sequence includes
 CC regions that are conserved throughout the various nAChR alpha
 CC subunits and which are essential for ligand binding. The invention
 CC relates to water-soluble ligand-binding proteins derived from
 CC molluscs, especially acetylcholine-binding proteins (AChBPs) and
 CC analogues of ligand-gated ion channels, their crystals, and their
 CC use for screening ligands of ligand-gated ion channels. The
 CC water-soluble ligand-binding proteins are capable of forming
 CC multimers and are amenable to crystallization. The crystal
 CC structure of AChBP is provided, and can be used to generate 3D
 CC models of the extracellular ligand-binding domain of ligand-gated
 CC ion channels and thus for screening of drugs that act on these
 CC ion channels. Chimeric proteins are provided that are capable of
 CC binding a ligand of a ligand-gated receptor, and comprise at
 CC least the amino acids of the AChBP determining solubility of the
 CC AChBP, in the same positions as in the AChBP, and also comprising
 CC amino acids determining binding to the ligand. In the chimeric
 CC conserved regions of an nAChR have been substituted for the
 CC corresponding amino acids, and preferably entire stretches have
 CC been substituted. New drugs can be developed that selectively
 CC intervene in neuronal signalling pathways, especially where the
 CC ligand-gated ion channel is the nAChR, and the related disorder is
 CC Tourette's syndrome, Alzheimer's disease, addiction to nicotine
 CC or schizophrenia.
 XX
 SQ Sequence 502 AA;

Query Match 28.7%; Score 1159.5; DB 22; Length 502;
 Best Local Similarity 45.1%; Pred. No. 1.4e-97;
 Matches 237; Conservative 82; Mismatches 115; Indels 91; Gaps 12;

QY 297 IYLNLSAK---VCLAGYHEKRLHDLDPYNTLPRVNLNESDPLQLSFLGLTLMQIDVDE 353
 DB 8 VMLAALASLLHVSLOGEFQRLKLYELVKNYPLRPVANDSQPLTVYFSLSLQIMDVE 67

QY 354 KNOILLVTNWLKLEWDMNLRWNTSDYGGVKDLRIPPHRIWKPVDVMTNSADEGFDGYQ 413
 DB 68 KNOVLTNWLQMSWTDHVQWNVSEYPCVKTVPFPGQIKWPKDILLNSADERFDATEFH 127

QY 414 TNVVRNNGSLYPPGIFKSTCKIDITWFFDDQRCCKMFGSWTYDGFQDLQLODETG 473
 DB 128 TNVLNNSGHCQYLPFGIFKSSCYIDVRWFPDVQHCCLKFGWSYGGWSLDQMQE--- 184

QY 474 GDISSYVLNGEWELLGVPCKNEIYNGCPPEYIDITFAIIRRTLYFFNLIIPCVLI 533
 DB 185 ADISCIYINGEWDLVGICRSERYECKPEYDPVTVVWRTLYIYGLNLLIPCVLI 244

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 21, 2003, 03:48:31 ; Search time 5045.31 Seconds
(without alignments)
11127.831 Million cell updates/sec

Title: US-09-303-232-1_COPY_372_2681

Perfect score: 2310

Sequence: 1 atgaaaatgcacaaactgaa.....caccacattattgtctgc 2310

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pin:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gsl1:*

29: gb_gsl2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	424.8	18.4	885	10	BG632919	BG632919 GH16126.3
2	332.2	14.4	1101	29	CNS000IF	AL058211 Drosophil
3	331.2	14.3	1007	29	CNS00HJU	AL073676 Drosophil
4	323.8	14.0	978	29	CNS006F9	AL064281 Drosophil

5	281.8	12.2	1201	9	AL530299	AL530299
6	265	11.5	607	9	AI292581	AI292581 GH15518.5
7	235.2	10.2	922	13	BU915857	AGENCOURT
8	232.6	10.1	2940	11	AK034228	Mus muscu
9	232.6	10.1	3230	11	AK083157	Mus muscu
10	228.8	9.9	833	14	CB245337	UI-M-FY0-
11	219.6	9.5	755	13	BU702422	UI-M-FY0-
12	219.2	9.5	4290	11	AK029177	Mus muscu
13	217	9.4	615	14	CB149460	K-EST0205
14	215.8	9.3	1864	11	AK053497	Mus muscu
15	215.8	9.3	2916	11	AK051730	Mus muscu
16	215.8	9.3	3126	11	AK080415	Mus muscu
17	207	9.0	3483	11	AK081254	Mus muscu
18	207	9.0	4037	11	AK049722	Mus muscu
19	207	9.0	4046	11	AK051742	Mus muscu
20	206.4	8.9	683	12	BM639954	170006876
21	205.4	8.9	908	13	BU149265	AGENCOURT
22	202.8	8.8	411	12	B1516733	B1516733
23	202.2	8.8	2010	11	AK080475	Mus muscu
24	201.8	8.7	410	12	B1516843	B1516843
25	200	8.7	658	12	BM711715	UI-E-CL1-
26	198	8.6	755	10	AW914206	EST345510
27	197.2	8.5	1036	13	BX437801	BX437801
28	196.6	8.5	2513	11	AK033068	Mus muscu
29	189.6	8.2	720	14	CA373069	CA373069
30	180.8	7.8	640	14	CB244439	UI-M-FY0-
31	178.8	7.7	1034	13	BX403124	BX403124
32	172.2	7.5	754	29	CNS02R2B	AI110117
33	170	7.4	891	9	AI110117	GH09582.5
34	169.8	7.4	882	12	B1195149	602944157
35	169.8	7.4	4589	11	AK030464	Mus muscu
36	168.8	7.3	763	14	CA374163	CA374163
37	168.4	7.3	600	13	BU919212	6021-01 M
38	154.8	6.7	809	10	BG404575	602420721
39	153.6	6.6	818	13	BU161024	AGENCOURT
40	153	6.6	586	13	BX299163	BX299163
41	152.2	6.6	1201	13	BX421718	BX421718
42	151.6	6.6	864	9	AU120692	AU120692
43	150.6	6.5	2342	11	AK009902	Mus muscu
44	146.6	6.3	494	9	AA697326	HL02253.5
45	146.4	6.3	694	12	B1194994	602944249

ALIGNMENTS

RESULT 1
BG632919/c

LOCUS
DEFINITION

BG632919 885 bp mRNA linear EST 23-APR-2001
GH16126.3prime GH Drosophila melanogaster head pot2 Drosophila
melanogaster cDNA clone GH16126 3 similar to CG4128: FBan0004128
'ion channel' located on: 2L 30D1-30E1;: 04/10/2001, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG632919

BG632919.1

EST.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 885)

Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,

Lewis,S. and Rubin,G.M.

BDGP/HMI Drosophila EST Project

Unpublished

Other_ESTs: GH16126.5prime

Contact: Stapleton, M.

BDGP

Lawrence Berkeley National Lab

One Cyclotron Rd, Berkeley, CA 94720, USA

Fax: 510 486 6798

Email: <http://www.fruitfly.org/EST>, est@fruitfly.berkeley.edu

Based upon the presence of a XhoI site followed by a run of 14 or

Db 413 GATGAAGTTCCGAGTTGACCTACGAGGATTCCAGGT 451
 |||||

RESULT 3

CNS000HJU

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence TET3 end of BAC:
 BACR35F05 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

ACCESSION

AL073676

VERSION

AL073676.1

KEYWORDS

GSS.

SOURCE

Drosophila melanogaster (fruit fly)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 1007)

AUTHORS

Direct Submission

TITLE

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

JOURNAL

- Web : www.genoscope.cns.fr

COMMENT

Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammosier in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 p1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1..1007
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR35F05"
 /clone_lib="RPCI-98"
 /note="end : TET3"

BASE COUNT 255 a 230 c 246 g 271 t 5 others

ORIGIN

Query Match 14.3%; Score 331.2; DB 29; Length 1007;

Best Local Similarity 98.2%; Pred. No. 3.1e-69;

Matches 333; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY

1053 GCACGAGAAAATCAATTGCTAGTCACATAATGTGGTTAAACTGGAGTGAACGACAT 1112

Db

125 GCACGAGAAAATCAATTGCTAGTCACATAATGTGGTTAAACTGGAGTGAACGACAT 184

QY

1113 GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTCGGAATACCCCGCA 1172

Db

185 GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTCGGAATACCCCGCA 244

QY

1173 TCGCATCTGGAAGCCGGAGCTGCTGATGTACACAGTCGGGATGAGGATTTGACGGCAC 1232

Db

245 TCGCATCTGGAAGCCGGAGCTGCTGATGTACACAGTCGGGATGAGGATTTGATGGCAC 304

QY

1233 CTACACAGACGACGTTGGTGGCGGAACAACGGCTGCTGTATACGTTCCGCGGGAT 1292

Db

305 CTACACAGACGACGTTGGTGGCGGAACAACGGCTGCTGTATACGTTCCGCGGGAT 364

QY

1293 CTTCAAGTCGACGTCGAAGATCGACATCAGCTGGTTCCCTTCGATGACACGCGGTGCGA 1352

Db

365 CTTCAAGTCGACGTCGAAGATCGACATCAGCTGGTTCCCTTCGATGACACGCGGTGCGA 424

QY 1353 GATGAAGTTCCGAGTTGACCTACGAGGATTCCAGGT 1391

|||||

Db 425 GATGAAGTTCCGAGTTGACCTACGAGGATTCCAGGT 463

RESULT 4

CNS006F9

LOCUS

DEFINITION

Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR13K21 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

ACCESSION

AL064281

VERSION

AL064281.1

KEYWORDS

GSS.

SOURCE

Drosophila melanogaster (fruit fly)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

1 (bases 1 to 978)

AUTHORS

Direct Submission

TITLE

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

JOURNAL

- Web : www.genoscope.cns.fr

COMMENT

Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammosier in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 p1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

1..978
 /organism="Drosophila melanogaster"
 /mol_type="genomic DNA"
 /db_xref="taxon:7227"
 /clone="BACR13K21"
 /clone_lib="RPCI-98"
 /note="end : TET3"

BASE COUNT 249 a 221 c 236 g 260 t 12 others

ORIGIN

Query Match 14.0%; Score 323.8; DB.29; Length 978;

Best Local Similarity 99.1%; Pred. No. 1.9e-67;

Matches 336; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY

1053 GCACGAGAAAATCAATTGCTAGTCACATAATGTGGTTAAACTGGAGTGAACGACAT 1112

Db

117 GCACGAGAAAATCAATTGCTAGTCACATAATGTGGTTAAACTGGAGTGAACG-CAT 175

QY

1113 GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTCGGAATACCCCGCA 1172

Db

176 GAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTAAGGATCTCGGAATACCCCGCA 235

QY

1173 TCGCATCTGGAAGCCGGAGCTGCTGATGTACACAGTCGGGATGAGGATTTGACGGCAC 1232

Db

236 TCGCATCTGGAAGCCGGAGCTGCTGATGTACACAGTCGGGATGAGGATTTGATGGCAC 295

QY

1233 CTACACAGACGACGTTGGTGGCGGAACAACGGCTGCTGTATACGTTCCGCGGGAT 1292

Db

296 CTACACAGACGACGTTGGTGGCGGAACAACGGCTGCTGTATACGTTCCGCGGGAT 355

QY

1293 CTTCAAGTCGACGTCGAAGATCGACATCAGCTGGTTCCCTTCGATGACACGCGGTGCGA 1352


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356 CTTCAAGTCGAGTCGCAAGATGACATCAGTGGTTCCTTCGATGACACCGGTGCGA 415
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1353 GATGAAGTTCGGCAGTTGGACCTAGCAGCGATTCCAGCT 1391
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416 GATGAAGTTCGGCAGTTGGACCTAGCAGCGATTCCAGGT 454
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AL530299 1201 bp mRNA linear EST 23-MAY-2003
AL530299 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CS0DD007YP05 5-PRIME, mRNA sequence.
AL530299
AL530299.2 GI:31068132
EST.
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12793792.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7646.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DD007CH030P1&cluster=7646.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DD007CH03Qp1.
Location/Qualifiers
1. 1201
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/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 258 a 326 c 319 g 273 t 25 others
ORIGIN
Query Match 12.2%; Score 281.8; DB 9; Length 1201;
Best Local Similarity 59.8%; Pred. No. 3e-57;
Matches 503; Conservative 5; Mismatches 322; Indels 11; Gaps 2;

QY 905 CTGCTAAAGTTGCCCTAGCAGGATATCATGAAAAGAGACTGTGTACACGATCTTTGGATC 964
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170 CTCCTCAGCGTGTCCCTGCAAGCGAGTCCAGAGGAAGCTTTACAGGAGCTGGTCAAGA 229
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|||||
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290 CCTGAGCCTCTGCGAGATCATGGAGTGTGATGAGAGAACCAAGTTTAAACCACCAACA 349
|||||
QY 1085 TGTGGTTAAACTGGAGTGAACGACATGAATCTCCGCTGGAGAACACCTCCGACTATGGCG 1144
|||||
350 TTTGGCTGCAAAATGCTCTTGACAGAGATCACTATTATACAGTGAATGTGTGAGAAATATCCAG 409
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QY 1145 GAGTTAAGGATCTGCGCAATACCCGCCATCGCATCTGGAAGCGGACGTGCTCATGTACA 1204
|||||

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|||||
410 GGGTGAAGACTTTCGTTTCCAGATGGCCAGATTGGAAACAGACATCTTCTCTATA 469
|||||
1205 ACAGTGGGATGAGGATTTGACGACACCTACACAGAAAGCTGGTGGTGGGAAACAAG 1264
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470 ACAGTGTGATGAGCGCTTTGACGCCACATTCACACACTACCGTGTGGTGAATCTCTG 529
|||||
1265 GCTCGTGTATACGTTCCGCCGGGATCTTCAAGTCGACGTCGACGATCGATCAGCT 1324
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530 GGCATTGGCAGTWCCTGCCCTCCAGGACATATTCAAGAGTTCCCTGCTACATCGATGACGCT 589
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701 ATGGAGAATGGACCTAGTGGGAATCCCGGCAAGAGAGTGAAGGTTCTATAGTCT 760
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1505 GCCCGGAACCTATATAGACATCACCCTCGCCATCATATCCCGGACGAGAGCTACT 1564
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761 GCAAGAGCCCTACCCCGATGTACCTTCACAGTGACCATGCGCGCAGAGCGCTCTACT 820
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1565 ATTCTTCAACCTGATACATCTGTGTACTGATTCCTTCATGCTTCCTTCGATGCTCA 1624
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821 ATGGGCTCAACCTGCTGATCCCTGTGTGCTCATCTCCGCCCTCGCCCTGCTGTTCC 880
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1625 CCTCGCCGCGAGATTC--GGGTGAAATATTCGTGGTGGTGTGTACATCTTCTCTCTCT 1682
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881 TCGTTCTCGACATTCGGGGGAGAAGATTTCCCTKGGGATAACAGTATTACTCTCTCT 940
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1683 GACCGTGTTCGATATGTTGCCGAGACATCCGCGTACTTCGATGCGGTGCGCAT 1742
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1743 G 1743
|
1001 G 1001

RESULT 6
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LOCUS GH15518.5prime GH Drosophila melanogaster head pot2 Drosophila
DEFINITION melanogaster cDNA clone GH15518 5 similar to CG4128: FBan0004128
'ion channel', located on: 2L 30D1-30E1;; 04/10/2001, mRNA sequence.
ACCESSION AI292581
VERSION AI292581.1 GI:3941988
KEYWORDS EST.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 607)
AUTHORS Harvey, D., Brokstein, P., Hong, L., Evans-Holm, M., Su, C., Tsang, G.,
Lewis, S. and Rubin, G. M.
BDGP/HMI Drosophila EST Project
Other_ESTS: GH15518.3prime
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AB003626; arm:2L [9617316.9882551]
estimated-cyto:30C7-30F4; 04/10/2001
Plate: GH.155 row: B column: 6

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QY	1651	TTATCGCTGGGTTTACCATCTTCTCGCTGACCGTGTTCGTGAATATGGTTGCCGAG	1710
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QY	1711	ACAATGCGCGCTACTTCCGATCGCGGTGCCATT	1742
Db	688	ATTATGCCAGCAACCTCAGACTCTGTCCCACT	719
RESULT	8		
LOCUS	AK034228		
DEFINITION	Mus musculus adult male diencephalon cDNA, RIKEN full-length enriched library, clone:9330165116 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.	2940 bp	linear
ACCESSION	AK034228		
VERSION	AK034228.1		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20493374		
PUBMED	11042159		
REFERENCE			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuami, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujitake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanishi, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE			
AUTHORS	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamana, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nika, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Anono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.		
TITLE	Functional annotation of a full-length mouse cDNA collection		
JOURNAL	Nature 409 (6821), 685-690 (2001)		
MEDLINE	21085660		
QY	11217851		
REFERENCE	5		
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		
JOURNAL	Nature 420, 563-573 (2002)		
REFERENCE	6 (bases 1 to 2940)		
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kaya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akaira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ Location/Qualifiers		
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ORIGIN			
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Best Local Similarity	56.6%;	Pred. No. 3.2e-45;	Length 2940;

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Qy	989	TTCTCAATGAATCGGACCGGTTACAAATTAAGCTTTGGTTTAACTTTAAATGCAATATCG	1048							
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Db	525	TCACCACCTTAACAAAGCCACCTGTTCTATGATGGCGTGTGCGAGTGACACCCCGG	584							
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Qy	1409	ATGAACCTGCGGTGATATCAGCAGTTACTGTCTCAAGCGGAGTGGGAAGTACTGGGTG	1468							
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Qy	1529	CCTTCCGCATCATATCCGCGGACGAACTGTACTATTCTTCAACCTGATCACTT	1588							
Db	822	CCTACGCTTCATCATCCGCGGACTCCCACTGTTCTACACCACTTATCATCCCT	881							
Qy	1589	GTCTACTGATTCCTCCATGGCTTCTCGGATTCACCTGCGCGAGATTCGGGTGAA	1648							
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Qy	1649	AATTATCGCTGGGTGTTTACCATCTTGCTCTCGCTGACCGGTGTTCTGAATATGGTTGCGG	1708							
Db	942	AGTCAAGCTGTGCATCTCGGTGCTGTTTCTCTACCGCTTCTGCTGCTCATCACCG	1001							
Qy	1709	AGACAATGCGCGTACTTC	1727							
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RESULT 9										
AK083157										
LOCUS										
DEFINITION										
Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:C630019w18 product:cholinergic receptor, nicotinic, alpha polypeptide 4, full insert sequence.										
ACCSSION										
VERSION										
KEYWORDS										
SOURCE										
ORGANISM										
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.										
REFERENCE										
1										

AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE

AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE

TITLE
JOURNAL
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REFERENCE

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MEDLINE
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PUBMED
REFERENCE

TITLE
JOURNAL

Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636

2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159

3
Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861

4
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fieischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Balderelli, R., Barsh, G., Blake, J., Boffelli, P., Bojunga, N., Carninci, P., de Bona, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohtsuki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851

5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3230)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsumi, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC),

[illegible]

```

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ACCESSION CB149460
VERSION   CB149460
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SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 615)
AUTHORS  Kim, N.S., Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim, M. R.,
Oh, K. J., Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. and
Kim, Y. S.
TITLE    21C Frontier Korean EST Project 2001
JOURNAL  Unpublished
COMMENT  Contact: Kim YS
        Genome Research Center
        Korea Research Institute of Bioscience & Biotechnology
        52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
        Tel: +82-42-860-4470
        Fax: +82-42-860-4409
        Email: yongsung@mail.kribb.re.kr
        Plate: 50 row: D column: 08
        High quality sequence stop: 615.
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                with tabacco acid pyrophosphatase (TAP). The decapped
                intact mRNA was ligated with DNA-RNA linker including
                EcoRI site by treatment of T4 RNA ligase and the first
                strand cDNA was synthesized from oligo dT-selected mRNA by
                priming with dr-tailed vector. The dr-tailed vector was
                adjusted to have about 60nt. The cDNA vector was
                circularized with E. coli DNA ligase after digestion of
                EcoRI which site is also included in vector. An RNA strand
                converted to a DNA strand by Okayama-Berg method. The
                obtained cDNA vectors were used for transformation of
                competent cells E. coli Top10f' by electroporation method.
                The cDNA libraries constructed by this method are
                full-length enriched cDNA library."
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BASE COUNT
ORIGIN

Query Match

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Matches 347; Conservative 0; Mismatches 185; Indels 9; Gaps 1;

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D 1 CGATATGCTGATAAACCTTTGACGCCACATTCACACTAACGTGTGGTGAATTCCTC 60

QY 1263 CGGCTCGTGCTATACGTTCGCGCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCAC 1322
D 61 TGGCATTGGCCAGTACCTGCGCTCCAGGCATATTCAGAGTTTCTCTACATCGATGTACG 120

QY 1323 GTGGTTCCTTCGATGACACCGGTCGGAGATGAAGTTCCGCGAGTTGGACCTAGCAGCG 1382
D 121 CTGGTTTCCCTTGTATGTCGACGACTGCAAACTGAAGTTTGGTCTTACGGAGG 180

QY 1383 ATTCAGCTGGATTTACAAATTACAAGATGAAGTGGCGGTGATATCAGCAGTTACGTGCT 1442
D 181 CTGGTCTTGGATCTGCAGATGCAGAGGCA-----CATATCAGTGGCTATATCCC 231

QY 1443 CAACGGCGAGTGGGAATCTACTGGTGTGCGCGCAACGTAACGAGATCTATTACAACGTG 1502
D 232 CAATGGAGAATGGGACCTACTTGGGAATCCCGCGCAAGAGGAGTGAAGGTTCTATGAGTG 291

QY 1503 CTGCGCGGAACCTTATAGACATCACCTTCGCCATCATCATCCGCGACGACAACTGTA 1562
D 292 CTGCAAGAGGCGCTACCCCGATGTCACCTTCACAGTGACCATGCGCGCAGGACACTCTA 351

QY 1563 CTATTTCTTCAACCTGATCATACCTTGTTGTAATGATTCCTCCATCCGCTGCTCGGAT 1622
D 352 CTATGGCTCAACCTGCTGATCCCTGTGTCTCATCTCCGCGCTGCTGCTGCTT 411

QY 1623 CACCTGCGCGCAGATTCGGTGGTGAATAATATCGTGGGTGTATACCATCTTGTCTGCTGCT 1682
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LOCUS
DEFINITION
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AK053497
AK053497.1 GI:26343494
HTC; CAP trapper.
Mus musculus (house mouse)

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
10349636
2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

QY 20499374
D 11042159
REFERENCE
AUTHORS
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,

Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (KISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL
MEDLINE
PUBMED
20530913
11076861
4

REFERENCE
AUTHORS
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yananaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaado,I., Pesole,G., Sackebush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Balderelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seva,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilmink,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)

JOURNAL
MEDLINE
PUBMED
21085660
11217851
5

REFERENCE
AUTHORS
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)

QY 563 G 532
D 532 G 532

6 (bases 1 to 1864)

ADACHI,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome-gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome-gsc.riken.go.jp/ Location/Qualifiers 1. 1864 /organism="Mus musculus"

Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzairelli,J., Mombaerts,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyooka,K., Wang,K.H., Weltz,C., Whittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409 (6821), 685-690 (2001)

MEDLINE 21085660

PUBMED 11217851

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2916)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

FEATURES Please visit our web site for further details.

source URL:http://genome.gsc.riken.go.jp/

FEATURES Location/Qualifiers

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putative

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Db 253 TGAGCACCGCTGTTCACGATACCTCTTTTGAAGATTACAACAGAGATCATCCGCGCGTGGC 312

QY 993 CAATGAATCGGACCGGTTTACAATTAAGCTTTTGGTTTAACTTTAATGCAAAATATCATGAT 1052

Db 313 TAACGTGTCCCATCCTGTCTATCCATCCAGTTTGGAGTGTCTATGTCTCAGCTGGTGAAGGT 372

QY 1053 GGACGAGAAAAATCAATTTGCTAGTCACPAATGTGTGGTTAAAACTGGAGTGAACGACAT 1112

Db 373 GGATGAAGTAACACAGATCATGGAACCAACCTGTGGCTGAACAAATCTGGAATGACTA 432

QY 1113 GAATCTCCGCTGGACACCTCCGACTATGGCGGAGTTAAGGATCTGCGAATACCGCCGCA 1172

Db 433 CAAGCTGAATGGAAACCTCTGCTACCAAGGGGTGGAGTTTCATGCGAGTCCCTGCGAGA 492

QY 1173 TCGCATCTGGAAGCGGAGCTGCTGATGTACAACTGCGGATGAGGATTTGACGCGAC 1232

Db 493 GAAGATCTGGAACACAGACATCGTCTTTTACAACACCGCGATGGGATTTCCAAAGTGA 552

QY 1233 CTACAGACGAACGCTGGTGGTGGCGGAACAACGGCTCTGTCTATACGTTCCGCGCGGAT 1292

Db 553 TGACAAACCAAGCTCTACTCAAGTACACAGGAGAAGTGAAGTCTGATCCCTCCGCGCAT 612

QY 1293 CTTCAAGTCGAGGTGCAAGATCGACATCACTGCTTCCCTTCGATGACGAGGCTGGGA 1352

Db 613 CTTTAAAGAGCTCATGCAAAATCGATGACCTACTTCCCTGTTGACTACCAAACTGCAC 672

QY 1353 GATGAAGTTCGCGAGTTCGACCTAGCAGCGGATTCAGCTGGATTTTACAATTAACAAGATGA 1412

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Db 790 GGGCTACAAACATGAATCAAGTACAACTGTGTGAGGAGATCTTACCAAGACATCACGTA 849

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Db 850 CTCGCTATACATCCGCGCTGCGCTGTCTTACACCATCAACCTCATCATCTCCGTGCT 909

QY 1593 ACTGATTCCTCCATGGCTTGTCTGGATTCAACCTGCGCGCAGATTCGGGTGAAAAAT 1652

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QY 1713 AATGCGGCTACTTCCGATGCGGTGCCATTG 1743

Db 1030 CATCCCTTCCACTCATCTGGTCTATCCCTTTG 1060

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	531	23.0	803	23	ABL07799
5	512.8	22.2	3700	21	AAZ24476
6	479	20.7	936	23	ABL13733
7	412.2	17.8	1540	23	ABL07231
8	411.4	17.8	3109	21	AAZ24477

9	335.8	14.5	14668	23	ABL07798	Drosophila melanog
10	296.2	12.8	1509	21	AAZ58395	Human PRO2145 nucl
11	296.2	12.8	1509	22	AAC90380	Wild-type human al
12	296.2	12.8	1876	15	AAV12197	Human neuronal nic
13	296.2	12.8	1876	18	AAZ48239	Human neuronal nic
14	296.2	12.8	1876	24	ABV73248	Human neuronal NAC
15	296.2	12.8	1876	24	ABS54875	Human neuronal nic
16	294.6	12.8	1509	22	AAC90385	Mutant human alpha
17	294.6	12.8	1509	22	AAC90386	Mutant human alpha
18	294.6	12.8	1509	19	AAV44687	V274T variant huma
19	293	12.7	1509	22	AAC90387	Mutant human alpha
20	284.4	12.3	2101	18	AAZ59197	Neuronal alpha-bun
21	283.8	12.3	1964	24	ABZ11298	Human polynucleoti
22	267.8	11.6	2769	18	AAZ59196	Neuronal alpha-bun
23	251	10.9	2277	15	AAV12199	Human neuronal nic
24	251	10.9	2277	16	AAQ90387	Alpha 2 subunit of
25	251	10.9	2277	24	ABV73243	Human neuronal NAC
26	251	10.9	2277	24	ABS54870	Human neuronal nic
27	251	10.9	2664	18	AAT48235	Neuronal nicotinic
28	251	10.9	2664	24	ABK92165	Prostate cancer-as
29	245.6	10.6	1416	22	AAC90382	Chimeric alpha7/5-
30	242.6	10.5	1809	23	AAS91552	DNA encoding novel
31	242.6	10.5	2082	18	AAT59527	Alpha4 subunit of
32	242.6	10.5	3496	18	AAT48237	Neuronal nicotinic
33	241.2	10.4	2398	23	ABL26491	Drosophila melanog
34	241	10.4	2082	18	AAT59528	Alpha4 subunit of
35	240.8	10.4	1869	24	AAL45873	Modified acetylcho
36	240.8	10.4	1869	24	ABL54794	Modified hen ACR s
37	234.8	10.2	2319	23	ABL04391	Drosophila melanog
38	233	10.1	2210	23	ABL10275	Drosophila melanog
39	232.4	10.1	1896	24	AAL45867	Modified acetylcho
40	231.4	10.0	2363	15	AAV12196	Human neuronal nic
41	231.4	10.0	2363	24	ABV73245	Human neuronal NAC
42	231.4	10.0	2363	24	ABS54872	Human neuronal nic
43	228	9.9	1869	24	AAL45864	Modified acetylcho
44	228	9.9	1869	24	ABL54788	Insect nicotinic A
45	225.6	9.8	1908	18	AAT48236	Neuronal nicotinic

ALIGNMENTS

RESULT 1
AAZ24475
ID AAZ24475 standard; CDNA to mRNA; 2886 BP.
XX
AC AAZ24475;
XX
DT 17-FEB-2000 (first entry)
XX
DE D. melanogaster acetyl-choline receptor DNA from clone Da7.
XX
KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
KW neurotransmission; plant protection agent; conductance; AChR; ds.
XX
OS Drosophila melanogaster.
XX
FH Key Location/Qualifiers
CDS 372..2684
FT /*tag_a
FT /product="acetyl choline receptor."
XX
PN DE19819829-A1.
XX
PD 11-NOV-1999.
XX
PF 04-MAY-1998; 98DE-1019829.
XX
PR 04-MAY-1998; 98DE-1019829.
XX
PA (FARB) BAYER AG.
XX
PI Adamczewski M, Oellers N, Schulte T;

QY 1801 GGACGACCGCTGATCCTAGAGTTCCGACACCGCCCTGTTGAGACACATCCTCCGAGCG 1860
DB 2172 GGACGACCGCTGATCCTAGAGTTCCGACACCGCCCTGTTGAGACACATCCTCCGAGCG 2231
QY 1861 AAGCACCAGATCTCTCCGACGTTGAGCTGAAGAGCGCTGTCGAAATCGTGTGGCC 1920
DB 2232 AAGCACCAGATCTCTCCGACGTTGAGCTGAAGAGCGCTGTCGAAATCGTGTGGCC 2291
QY 1921 AAGCTACTAGACATCGATGATGACTTCCGGCACAATTGTCGCCCATGACGCCGCGGA 1980
DB 2292 AAGCTACTAGACATCGATGATGACTTCCGGCACAATTGTCGCCCATGACGCCGCGGA 2351
QY 1981 ACACCTGCCACACACCCGCGCTTCTATCGCAGGTTTATGGACAAGCGCGATGCGCAGC 2040
DB 2352 ACACCTGCCACACACCCGCGCTTCTATCGCAGGTTTATGGACAAGCGCGATGCGCAGC 2411
QY 2041 ATTGGGCCAATTGGCAGACCCGATGCGGATGCGGTCACCCATCATACGTCGATCAAA 2100
DB 2412 ATTGGGCCAATTGGCAGACCCGATGCGGATGCGGTCACCCATCATACGTCGATCAAA 2471
QY 2101 TCATCAACTGAATATCAATAGTGTAAATCTTAAAGGAAATTCGCTTTTAACTGATCAG 2160
DB 2472 TCATCAACTGAATATCAATAGTGTAAATCTTAAAGGAAATTCGCTTTTAACTGATCAG 2531
QY 2161 CTACGTPAAGATGACGAGTCAATGACATGCGCAATGATGGCAATTTGCAAGCTATGTC 2220
DB 2532 CTACGTPAAGATGACGAGTCAATGACATGCGCAATGATGGCAATTTGCAAGCTATGTC 2591
QY 2221 GTTGACAGACTGTGCTTATCATATTCACAATGTTGCAATATTAGCCACAATAGCTGA 2280
DB 2592 GTTGACAGACTGTGCTTATCATATTCACAATGTTGCAATATTAGCCACAATAGCTGA 2651
QY 2281 CTACTATCGGCACCATATATTGTCGTCG 2310
DB 2652 CTACTATCGGCACCATATATTGTCGTCG 2681

RESULT 2

ABL27131
ID ABL27131 standard; DNA; 984 BP.
AC ABL27131;
XX
XX 26-MAR-2002 (first entry)
DT
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 32866.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
OS
XX WQ200171042-A2.
XX
XX 27-SEP-2001.
PD
XX 23-MAR-2001; 2001WO-US09231.
PF
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
PI
XX WPI; 2001-656860/75.
DR
XX . New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Claim 1; SEQ ID NO 32866; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 984 BP; 332 A; 268 C; 225 G; 159 T; 0 other;

Query Match 38.1%; Score 881; DB 23; Length 984;
Best Local Similarity 98.0%; Pred. No. 1.4e-235;
Matches 903; Conservative 0; Mismatches 15; Indels 3; Gaps 1;

QY 1 ATGAAAATGCACAACTGAACTGACTGAAGTTGACGATGATGAGCTGTGGCTGGCAGTA 60
DB 1 ATGAAAATGCACAACTGAACTGACTGAAGTTGACGATGATGAGCTGTGGCTGGCAGTA 60
QY 61 AGATTAGCGACTGCGAGCAGCAACTTTAGCAGCAGTAGCAGCACAAGACCACCCAGCAGC 120
DB 61 AGATTAGCGACTGCGAGCAGCAACTTTAGCAGCAGTAGCAGCACAAGACCACCCAGCAGC 120
QY 121 AACACGAGCAGCAACACCGCAACTTCACACACTGCAACAGGAGCTTAAAGTACAAAACAC 180
DB 121 AACACGAGCAGCAACACCGCAACTTCACACACTGCAACAGGAGCTTAAAGTACAAAACAC 180
QY 181 CACAGCAACATTGCAAGCGAGCAGCAATAAGCAGCAACAGGAGCAGCAGATCGAAGGAC 240
DB 181 CACAGCAACATTGCAAGCGAGCAGCAATAAGCAGCAACAGGAGCAGCAGATCGAAGGAC 240
QY 241 GAGGATGAGCAACACCGCAACTTTAGCAGCAGTAGCAGCACAAGACCACCCAGCAGC 300
DB 241 GAGGATGAGCAACACCGCAACTTTAGCAGCAGTAGCAGCACAAGACCACCCAGCAGC 300
QY 301 AGCAGCAACATTGTTGCGCAAGACAGCGCGAGCAACTGCTGCCGCGATGAAGCA 360
DB 301 AGCAGCAACATTGTTGCGCAAGACAGCGCGAGCAACTGCTGCCGCGATGAAGCA 360
QY 361 ACAACCCAAACACCAACAACTAAGCTGTGTGCGCAAGCAGCAACAGATTCGCTGCG 420
DB 361 ACAACCCAAACACCAACAACTAAGCTGTGTGCGCAAGCAGCAACAGATTCGCTGCG 420
QY 421 CGACGAAAAGAAAACCCAGCAACCCCAAGCAAGATATCAAGAAACACCAACCAACTT 480
DB 421 CGACGAAAAGAAAACCCAGCAACCCCAAGCAAGATATCAAGAAACACCAACCAACTT 480
QY 481 AGCATGCTTCCCTTCAAAACCGCAACTTCACGAGCAGCACTTACAGCAGCAGCAACA 540
DB 481 AGCATGCTTCCCTTCAAAACCGCAACTTCACGAGCAGCACTTACAGCAGCAGCAACA 540
QY 541 ACCAGCTGTCGACAGCCACCTACATGCAATGTGAGCCAGCAGCAATGATTCAGTATT 600
DB 541 ACCAGCTGTCGACAGCCACCTACATGCAATGTGAGCCAGCAGCAATGATTCAGTATT 600
QY 601 CCGATATCGACATGATAGATATCCAGCGCCACATTCGCTGGCTGTGCTGCTGCTG 660
DB 601 CCGATATCGACATGATAGATATCCAGCGCCACATTCGCTGGCTGTGCTGCTGCTGCTG 660
QY 661 CAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 661 CAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
QY 721 CTGTTTCAGAGGATGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 780
DB 721 CTGTTTCAGAGGATGCGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 780
QY 781 GCGCAACTGAAAATAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 837
DB 781 GCGCAACTGAAAATAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 837

XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US09231.
 XX PR 23-MAR-2000; 2000US-191637P.
 XX PR 11-JUL-2000; 2000US-0614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR P-PSDB; ABB63696.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX PS Claim 1; SEQ ID NO 17879; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX SQ Sequence 803 BP; 211 A; 199 C; 190 G; 203 T; 0 other;

Query Match 23.0%; Score 531; DB 23; Length 803;
 Best Local Similarity 88.4%; Pred. No. 9.2e-138;
 Matches 616; Conservative 0; Mismatches 15; Indels 56; Gaps 1;

OY 1054 GACGAGAAATCAATGCTAGTCACTAATGTGTGTTAAACTGGAGTGAACGACATG 1113
 DB 1 GACGAGAAATCAATGCTAGTCACTAATGTGTGTTAAACTGGAGTGAACGACATG 60
 OY 1114 ATCTCCCTGGACACCTCCGACTATGCGGAGTTAAGGATCTCGAATACCGCGCAT 1173
 DB 61 ATCTCCCTGGACACCTCCGACTATGCGGAGTTAAGGATCTCGAATACCGCGCAT 120
 OY 1174 CGCATCTGGAAGCCGGAGTGTCTGATGTACACAGTGGGATGAGGGATTTGACGGCACC 1233
 DB 121 CGCATCTGGAAGCCGGAGTGTCTGATGTACACAGTGGGATGAGGGATTTGATGGCACC 180
 OY 1234 TACACAGAACAGTGGTGGTGGGAAACACGGCTCTGTCTATACGTTCCGCGGGGATC 1293
 DB 181 TACACAGAACAGTGGTGGTGGGAAACACGGCTCTGTCTATACGTTCCGCGGGGATC 240
 OY 1294 TTCAGTCCAGTGCAGATCGACATCAGTGGTGTCCCTTCGATGACACGGGTGCGAG 1353
 DB 241 TTCAGTCCAGTGCAGATCGACATCAGTGGTGTCCCTTCGATGACACGGGTGCGAG 300
 OY 1354 ATGAGTTCCGGAGTTGGACCTACGACGGATTTCCAGCTGGATTTACAATTACAAGATGA 1413
 DB 301 ATGAGTTCCGGAGTTGGACCTACGACGGATTTCCAGCTGGATTTCCAGTTGGT----- 343
 OY 1414 ACTGGCGGTGATATCAGCAGTTACGTGCTCAACGCGAGTGGGAACCTACTGGGTGCGCC 1473
 DB 344 -----TCAGTGTGCC 354
 OY 1474 GCGAACCTAGCAGATCTATTACAACCTGCTGCCCGAACCCCTATATAGACATCACCTTC 1533
 ||||||||||| ||||||||||| ||||||||||| ||||||||||| |||||||||||

DB 355 GCGAAACCTAACGAAATCTATTACAACCTGCTGCCGGAAACCCCTATATAGACATCACCTTC 414
 OY 1534 GCCATCATCATCCGCCGAGCAACACTGTACTATTCTTCAACCTGATCATACCTTTGTGTA 1593
 DB 415 GCCATCATCATCCGCCGAGCAACACTGTACTATTCTTCAACCTGATCATACCTTTGTGTA 474
 OY 1594 CTGATTGCTCCATGCGCCTTGGTCGGATTCAACCTGCGCGCAGATTCCGGTGAAATTA 1653
 DB 475 CTGATTGCTCCATGCGCCTTGGTCGGATTCACTCTGCGCGCAGATTCCGGTGAAATTA 534
 OY 1654 TCGCTGGGTGTACCATCTTCTCTCGCTGACCGGTGTTTCTCAATATGTTGCCGAGACA 1713
 DB 535 TCACCTGGGTGTACCATCTTCTCTCGCTGACCGGTGTTTCTCAATATGTTGCCGAGACA 594
 OY 1714 ATGCGCGCTACTTCCGATGCGGTGCGATTGTGGATAC 1750
 DB 595 ATGCGCGCTACTTCCGATGCGGTGCGATTGTGGATAC 631
 RESULT 5
 AA224476
 ID AA224476 standard; cDNA to mRNA; 3700 BP.
 XX AC AA224476;
 XX DT 17-FEB-2000 (first entry)
 XX DE H. virescens acetyl-choline receptor DNA from clone Hwa7-1.
 XX KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 KW neurotransmission; plant protection agent; conductance; AChR; ds.
 XX OS Heliothis virescens.
 XX FH Key Location/Qualifiers
 FT CDS 335..1825
 FT /*tag= a
 FT /product= "acetyl-choline receptor"
 XX DE19819829-A1.
 XX PD 11-NOV-1999.
 XX PF 04-MAY-1998; 98DE-1019829.
 XX PR 04-MAY-1998; 98DE-1019829.
 XX PA (FARB) BAYER AG.
 XX PI Adamczewski M, Oellers N, Schulte T;
 DR WPI; 2000-014207/02.
 DR P-PSDB; AAY50815.
 PT New nucleic acid encoding a nicotinic acetylcholine receptor from
 PT insects, used to identify potential insecticides -
 XX PS Claim 1a; Page 14-17; 26pp; German.
 CC This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (I) from insects which can be used as an
 CC insecticide. Inhibitors of (I) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant
 CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides, or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence encodes an acetyl-choline
 CC receptor isolated from Heliothis virescens.
 XX SQ Sequence 3700 BP; 893 A; 953 C; 944 G; 910 T; 0 other;

Query Match 22.2%; Score 512.8; DB 21; Length 3700;
Best Local Similarity 62.5%; Pred. No. 2.6e-132;
Matches 878; Conservative 0; Mismatches 502; Indels 24; Gaps 4;

Qy	925	GGATATCATGAAAGAGACTGTTACAGATCTTTTGGATCCTTATATACACTAGAACGT	984
Db	425	GGGTACACAGAGAGCGCTACTGCACACCTATTTGGACCACTACACGCTACTGGAGAGG	484
Qy	985	CCCGTCTCAATGAATCGGACCGTTCACAAATTAAGCTTTTGGTTAACTTTAAATGCAAAAT	1044
Db	485	CCCGTCTCAACAGAGACGACCGCTGCAGCTCTCCCTCGGCCTCAGCTCATGCGATC	544
Qy	1045	ATCGATGTGACGAGAAATCAATTTAGTACATTAATGTGTGGTTAAACATGGAGTGG	1104
Db	545	ATCGACGTGACGAGAGAACAGCTTTTAAACAAACATCTGGCTAAACATAGATGG	604
Qy	1105	AACGACATGAATCTCCGCTGGACACCTCCGACTATGCGGAGTAAAGATCTCGGNATA	1164
Db	605	AATGATATGAATTTGAGGTGGACACTTCAGATTTTCGGCGGGTCAAGATTTAAGAGTG	664
Qy	1165	CCGCGCATCGCATCTGGAAGCGGAGCTGCTGATGTACACAGTGGGATGAGGATTT	1224
Db	665	CCACCCACAGACTATGGAACACAGAGCTCTTATGTACAAACGCGGAGAGGTTTC	724
Qy	1225	GACGGCACCTACAGACGAGCTGGTGGTGGCGGAACAAACGGCTGTGTATACGTTCCG	1284
Db	725	GACAGCACGTATCCAAACGAGCTGGTGGTGGCGGAACAAACGGCTGTGTGTACGTCCG	784
Qy	1285	CCGGGGATCTCAAGTCAGCTCAAGATCGACATCAGCTGGTTCCCTTCGATGACCAG	1344
Db	785	CCGGGCATCTCAAGAGCACCTGCAAGATCGACATCAGCTGGTTCCCTTCGACGACCA	844
Qy	1345	CGGTGCGAGATGAATTTGCGAGTTGGACCTAGCAGGATTCAGCTGGATTTACAAATTA	1404
Db	845	CGATGCGAGATGAATTTGCGAGCTGACATTCATGATGTTATCAGTTGGATTCACACTA	904
Qy	1405	CAAGATGAATGCGGTGTATACAGAGTTAGCTGTCTCAACGCGAGTGGAGACTACTG	1464
Db	905	CAGGATGAAGGGCGGAGATATAAGCAGTTTGTCTACGAATGGCAATGGAGTTAATA	964
Qy	1465	GGTGTGCGCGCAACCTFAAGAGATCTATTACAACTGCTGCCGGAACCTATATAGAC	1524
Db	965	GGAGTCCCGCAGCGCAAGAGATCTACTACAACTGTTGTCCGAGCCATACATCGAC	1024
Qy	1525	ATCACCTTCGCGCATCATCCGCGCAGCAACACTGTACTATTCTTCAACCTGATCATA	1584
Db	1025	ATCACGTTTGGGTGGTATCCGAGAAACAGCTCTACTACTTCTTCAATCTGATCGTG	1084
Qy	1585	CTTTGTGTACTGATGCTCCATGGCCCTTGTCTGGATTCACCTGCGCGCAGATTCGGT	1644
Db	1085	CCCTGCTGTCTCATCGCTCCATGGCTCTATTGGGGTTCACTTGCCTCCAGACTCCGGA	1144
Qy	1645	GAAAAATATCGTGGGTGTATACATCTGTCTCTGCTGACCGGTCTTCTGAATATGTTT	1704
Db	1145	GAAAAATGTTTGTAGTGTGACGATATATCTGTGTGAGGTGTCTTCAACATGGTG	1204
Qy	1705	GCGGAGACAATTCGCGCTACTTCGATGCGGTGGCATTTG-----TGGATACGC	1752
Db	1205	GCGGAGAGATGCCAGCAGCTCGGACGCGTGGCCCTTGTTCGSCACCTACTTCAACTGC	1264
Qy	1753	ATCGTGTGTTTG--TGTGGTGGATGGATATTTGCAATGAGTCGCGCCAGGACCGC	1810
Db	1265	ATCATGTTTATGTTGGTGTCTCTCGCTGTCTCCACCATCTGATTCCTCAACTACCCAC	1324
Qy	1811	TGATCTTAGAGTTCCCGACACGCGCTTTCGGACACATCCTCCGACGGAA-----GCAC	1866
Db	1325	CGGACCGAGACACTCAGAAATGAGTGAATTTGATTCGTTGCTGTTTATTTGCTG	1384
Qy	1867	CAGATCTCTCCGAGTTGAGCTGAAAGAGCGCTGCTCGAAATCGCTGCTGGCCCAAGTA	1926
Db	1385	CCGTGGGTGCTGCGCATGTACGCGCCGCGGTGCGCGAGCAGCGCGCGCGCGCGGTA	1444
Qy	1927	CTAGACATCGATGATGACTTCCCGGCACAAATTTGTCGCCCCCATGAGCGCGCGGGAACACTG	1986

Db	1445	CTCCGCGCGCGACCTGGAGCTGCGCGAGCGCTCTCCAAAGTCGCTCTAGCGAACGTG	1504
Qy	1987	CCACACAACCCGCTTCTATATCGACGGTTTATGGACAAGCGCAGCATGGG	2046
Db	1505	CTCGACATCGATCAGCACTTCCGCCACCCCAAGCAGCAGCGCAATGCTGCCGATAC	1564
Qy	2047	CCAATTGGCAGCACCAGAAATGCGGATGCGGTCCACCATCATACGTGCAATCAATATCA	2106
Db	1565	TACAGGGGGGTGAGGAGATGCGCGGGGTGGCGCGCACAGTTGCTTC-----GGT	1618
Qy	2107	ACTGAATGAAATAGTTAATCTTAAAGAAATTCGCTTTTATACTGATCAGTACGT	2166
Db	1619	GTGCACTACAGCTCTCCCTCATTTCTGAAGGAGATTAGAGTCAATCAGATCAGATCGC	1678
Qy	2167	AAAGATGACCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG	2226
Db	1679	AAGAGACAGAAATGCGGACATTTGCGGCACTGGAAGTTCCGCCCATGCTGTGAC	1738
Qy	2227	AGACTGTGCTTATATTCACAAATGTTCCGCAATATAGCCACAATAGCTGACTACTA	2286
Db	1739	AGACTGTGCTTATATTTACCTTGTTCACAAATCATCGCACGCTAGCGCTGCTGCTG	1798
Qy	2287	TCGGCACCACATATTTGCTCTG 2310	
Db	1799	TCGGCACCACATCATGTTGCTG 1822	
RESULT 6			
ABLL3733			
ID	ABLL3733	standard; cDNA; 936 BP.	
XX	ABLL3733;		
XX	26-MAR-2002	(first entry)	
DE	Drosophila melanogaster	expressed polynucleotide SEQ ID NO 35681.	
KW	Drosophila; developmental biology; cell signalling; insecticide;		
KW	pharmaceutical; gene; ss.		
OS	Drosophila melanogaster.		
XX	WO200171042-A2.		
XX	27-SEP-2001.		
XX	23-MAR-2001;	2001WO-US09231.	
PR	23-MAR-2000;	2000US-191637P.	
PR	11-JUL-2000;	2000US-0614150.	
XX	(PEKE)	PE CORP NY.	
XX	Venter JC, Adams M, Li PWD, Myers EW;		
XX	WPI; 2001-656860/75.		
DR	P-PSDB; ABB69630.		
PT	New isolated nucleic acid detection reagent for detecting 1000 or more		
PT	genes from Drosophila and for elucidating cell signalling and cell-cell		
PT	interactions -		
XX	Claim 1; SEQ ID NO 35681; 2lpp + Sequence Listing; English.		
XX	The invention relates to an isolated nucleic acid detection reagent		
CC	capable of detecting 1000 or more genes from Drosophila. The invention is		
CC	useful in developmental biology and in elucidating cell signalling and		
CC	cell-cell interactions in higher eukaryotes for the development of		
CC	insecticides, therapeutics and pharmaceutical drugs. The invention		
CC	discloses genomic DNA sequences (ABLL16176-ABLL30511), expressed DNA		
CC	sequences (ABLL1840-ABLL16175) and the encoded proteins		
CC	(ABBS57737-ABBS72072).		

QY 1269 GTGCTATAGTTCCTCCCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCAGTGGTT 1328
 Db 466 TTGCTGTAGTGCCTCCCTGGTATCTTCAAGACCATGCAAGATGACATCAGTGGTT 525
 QY 1329 CCCTTCGATGACACGGGTGCGAGATGAAGTTGCGCAGTTGGACCTACACGAGTTCCA 1388
 Db 526 CCATTTGATGACCAACATTCGGAATGAATTCGGTAGTTGGACITACGATGGAATCA 585
 QY 1389 GCTGGATTTACAATTAACAAGATGAACCTGGCGGTGATATACGAGTTTACGTGCTCAACGG 1448
 Db 586 GTTGGATTTGGTTTGAATTCGGAAGATGAGGGGATCTTTCCGATTTTCAACAATGG 645
 QY 1449 CGAGTGGAACTACTGGGT---GTGCCCCGGAACGTAACGAGATCTATTAACAAGTCT 1504
 Db 646 CGAGTGGTACTTGGTTTACCATTGCGGGGAAGAAGATACGATAGTCTACGCCCTGCT 705
 QY 1505 GCCCGGAACCTATATAGATACATCACCCTTCGCCATCATCCGCGGACGAACTGTACT 1564
 Db 706 GCCCAGAACCATATGTCATATACCTTTACTATACAAATTCGTGCGCGGTACATATATT 765
 QY 1565 ATTCTTCAACCTGATCATACCTTGTGTACTGATTCCTCCATGGCTTCTCGGATTTCA 1624
 Db 766 ATTTTTCATTTAATTTGTCATGTCTGCTAATCTCATCGATGGCCCTACTGGCTTCA 825
 QY 1625 CCCTGCCCGCAGATTCGGGTGAATAATATCGTGGGTGTACCATCTTCTCGCTGA 1684
 Db 826 CATTCGCCCGGATTCGGCGGAGAACTGACGTGGCGGTAACTATATCTACTATCAPTAA 885
 QY 1685 CCGTGTCTTGAATATGTTGCCGAGACAATGCCGCTACTTCCGATGCGGTGCC 1739
 Db 886 CAGTATTTCTAACTTGTCCGAGTCCATGCCGACAACGTGGATGCTGTTC 940

RESULT 8

AAZ24477
 ID AAZ24477 standard; cDNA to mRNA; 3109 BP.

XX AC AAZ24477;

XX DT 17-FEB-2000 (first entry)

XX DE H. virescens acetyl-choline receptor DNA from clone Hva7-2.

XX KW Acetyl-choline receptor; nicotinic; insect; insecticide; screening;
 KW neurotransmission; plant protection agent; conductance; AChR; ds.

XX OS Heliothis virescens.

XX PN DE19819829-AL.

XX PD 11-NOV-1999.

XX PF 04-MAY-1998; 98DE-1019829.

XX PR 04-MAY-1998; 98DE-1019829.

XX PA (FARB) BAYER AG.

XX PI Adamczewski M, Oellers N, Schulte T;

XX DR WPI; 2000-014207/02.

XX P-PSDB; AAY50816.

XX PT New nucleic acid encoding a nicotinic acetylcholine receptor from
 XX insects, used to identify potential insecticides -

XX PS Claim 1a; Page 19-22; 26pp; German.

XX This invention describes a novel nucleic acid (NA) encoding a nicotinic
 CC acetyl-choline receptor (r) from insects which can be used as an
 CC insecticide. Inhibitors of (r) interfere with neurotransmission. (I)
 CC (also vectors containing it, its regulatory regions, and antibodies
 CC directed against (I)-encoded proteins) are used to screen for: (a) plant

CC protection agents that alter conductance of AChR, potentially useful as
 CC insecticides, or (b) genes which encode polypeptides that are involved in
 CC formation of functionally related AChR in insects. (I) are also used to
 CC isolate and characterize the specified regulatory regions and for
 CC recombinant production of (II). This sequence encodes an acetyl-choline
 CC receptor isolated from *Heliothis virescens*.
 XX
 SQ Sequence 3109 BP; 923 A; 610 C; 742 G; 834 T; 0 other;

Query Match 17.8%; Score 411.4; DB 21; Length 3109;
 Best Local Similarity 68.8%; Pred. No. 5.3e-104;
 Matches 565; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 924 AGGATATCATGAAAAGAGACTGTTACACGATCTTTTGGATCCCTTATATACACTAGAACG 983
 Db 151 AGGTCTCTACGAGAAGAGACTCTCTGAACGGTGTCTGGCGAACTACAAACCCCTGGAGCG 210
 QY 984 TCCCGTCTCAATGAATCGGACCCGTTACAATTAAGCTTTGGTTTAACTTTAATGCAAT 1043
 Db 211 ACCGGTGGCCACGAGAGCGAACCGCTAGAGGTGACGTTTGGCTTGCACCTTGCAGCAAT 270
 QY 1044 TATCGATGTGGACGAGAAAATCAATTCGTAGTCACTAATGTGTGGTTAAAACCTGGAGTG 1103
 Db 271 CATTCAGCTGGACGAGAAGATCAACTACTTATAACCAATATATGGCTGCTGTGGAGTG 330
 QY 1104 GAACGACATGAATCTCCGCTGGAAACCTCCGACTATGGCGGAGTTAAGGATCTGCGAAT 1163
 Db 331 GAATGACTACAACCTGAGGTGGAAACGACGAGTATGGCGGGTCAAGGACCTCAGGAT 390
 QY 1164 ACCGCCCATCGCATCTGGAAGCGGACGTGCTGATGTACAACAGTCGGATGAGGATTT 1223
 Db 391 CACGCCCAACAAGTTGTGGAAGCGGACGTCTTATGTATATAGTCTGACGAGGTTT 450
 QY 1224 TGACGGCACCTACCAGACGACGTGTGTGGTGGGAAACAACGGCTGCTGTCTATACGTTCC 1283
 Db 451 TGACGGACCTACCAGACCAACGTTGGTGGTCAAGCGCGGCAAGTTGCGTGTACGTGCC 510
 QY 1284 GCGGGGATCTTCAAGTCGACGTGCAAGATCGACATCAGTGGTTCCTCCCTTCGATGACCA 1343
 Db 511 ACCTGGCATATTCAAGAGACATGCAAGATGGACATCGCGTGGTTTCCCTTCGACGACCA 570
 QY 1344 GCGGTGGAGATGAAGTTCGCGACTTGGACCTACGACGATTCACGCTGGATTTACAAT 1403
 Db 571 ACATGTGATATGAAGTTCGCTAGCTGGACATATGACGCAATCAGTTGGATCTGGTCT 630
 QY 1404 ACAAGTGAACCTGGCGGTGATATACGACTTACGTCTCAACGGCGAGTGGGAACCTACT 1463
 Db 631 AAAAGATGAGCAGGCGGCGATCTATCGGACTTCATAACAAATGGGAGTGGTATCTAAT 690
 QY 1464 GGGTGTGCCCGGAAACGTAACGAGATCTATTACAACCTGCTGCCCGGAAACCTATATAGA 1523
 Db 691 AGGAATGCCAGGCAAAAAGAACACAATAACATACGCGTGTGCCCGGAGCCCTACGTGGA 750
 QY 1524 CATCACCTTCGCCCATCATCATCCCGACCAACACTGTACTATTCTTCAACCTGATCAT 1583
 Db 751 CGTACCTTCACCATCATGATAAGAGACGAAACCTTGTACTTCTTCAACCTGATCGT 810
 QY 1584 ACCTTGTGTACTGATTCCTCCATGCTGCTGGATTCACCTCCCGGACAGATTCGGG 1643
 Db 811 CCGGTGGTCTGATCTCATCTGATGGCACTCCCTCGGCTTCACATCGCCACGAGCTCCG 870
 QY 1644 TGAAAAATATCGTGGGTGTTACCATCTTCTGCTCTCGCTGACCGCTGTTTCTGAATATGGT 1703
 Db 871 AGAGAACTCACACTTGGAGTCACTATTCTTCTATCGCTGACGCTGTTCTCTCAACCTGGT 930
 QY 1704 TGCCGAGACAATGCCGCTACTTCCGATGCGGTGCCATTGT 1744
 Db 931 AGCCGAGACCTGCGCACAGGTCTCCGACGTATCCCTCTGT 971

RESULT 9

ABL07798
 ID ABL07798 standard; cDNA; 14668 BP.

XX ABL07798;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 17876.
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX Drosophila melanogaster.
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656860/75.
XX P-PSDB; ABB63695.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX Claim 1; SEQ ID NO 17876; 21pp + Sequence Listing; English.
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABB57737-ABB72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 14568 BP; 4616 A; 3078 C; 2662 G; 4312 T; 0 other;
Query Match 14.5%; Score 335.8; DB 23; Length 14568;
Best Local Similarity 99.4%; Pred. No. 1.7e-82;
Matches 337; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1053 GGACGAGAAAATCAATTGCTACTACTATGTGTGTTAAACTGGAGTGAACGACAT 1112
DB 1000 GGACGAGAAAATCAATTGCTACTACTATGTGTGTTAAACTGGAGTGAACGACAT 1059
QY 1113 GAATCTCCCTGGAACACCTCCGACTATGCGGAGTTAAGGATCTCGGAATACCGCGCA 1172
DB 1060 GAATCTCCCTGGAACACCTCCGACTATGCGGAGTTAAGGATCTCGGAATACCGCGCA 1119
QY 1173 TCGCATCTGGAGCCGAGCTGCTGATGTACACAGTGGGATGAGGGATTTACGGCAC 1232
DB 1120 TCGCATCTGGAGCCGAGCTGCTGATGTACACAGTGGGATGAGGGATTTACGGCAC 1179
QY 1233 CTACACAGCAAGCTGTGTCGGGAACACGCTGCTGTCTATAGTTCCCGGGGAT 1292
DB 1180 CTACACAGCAAGCTGTGTCGGGAACACGCTGCTGTCTATAGTTCCCGGGGAT 1239
QY 1293 CTTCAAGTCGAGTCGAAGATCGACATCACGTGGTTCCTTCGATGACCGGTCGCA 1352
DB 1240 CTTCAAGTCGAGTCGAAGATCGACATCACGTGGTTCCTTCGATGACCGGTCGCA 1299
QY 1353 GATGAAGTTCGGAGTTGGACCTACGACCGGATTCAGCT 1391

DB. 1300 GATGAAGTTCGGAGTTGGACCTACGACCGGATTCAGCT 1338
RESULT 10
AAC58395
ID AAC58395 standard; cDNA; 1509 BP.
XX AAC58395;
XX 29-JAN-2001 (first entry)
XX Human PRO2145 nucleotide sequence SEQ ID NO:76.
XX Human; tumour; diagnosis; neoplastic disease; neoplastic cell growth;
XX proliferation; tumorigenesis; identification; cancer; cytostatic;
XX neoplastic; neuroprotective; antiinflammatory; immunosuppressive;
XX immunostimulant; antiangiogenic; leukaemia; lymphoid malignancy;
XX neuronal disorder; glioma disorder; astrocytoma disorder; angiogenic;
XX hypothalamic disorder; glandular disorder; macrophagal disorder;
XX epithelial disorder; stromal disorder; blastocoele disorder;
XX inflammatory disorder; immunologic disorder; ss.
XX Homo sapiens.
XX WO200053755-A2.
XX 14-SEP-2000.
XX 06-JAN-2000; 2000WO-US00376.
XX 08-MAR-1999; 99WO-US05028.
XX 02-JUN-1999; 99WO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 07-JUL-1999; 99US-0143048.
XX 26-JUL-1999; 99US-0145698.
XX 30-NOV-1999; 99WO-US28313.
XX 20-DEC-1999; 99WO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hillan KJ, Roy MA;
XX Watanabe CK, Wood WI;
XX WPI; 2000-572270/53.
XX P-PSDB; AAB24088.
XX Thirty PRO polynucleotides encoding PRO polypeptides, useful in the
XX treatment, diagnosis and prevention of cancer -
XX Claim 50; Fig 57; 286pp; English.
XX The present invention describes an isolated antibody that binds to
XX one of the human PRO proteins designated PRO212, PRO290, PRO341, PRO535,
XX PRO619, PRO717, PRO809, PRO830, PRO848, PRO943, PRO1005, PRO1009,
XX PRO1025, PRO1030, PRO1107, PRO1111, PRO1153, PRO1182, PRO1184,
XX PRO1187, PRO1281, PRO23, PRO39, PRO834, PRO1317, PRO1710, PRO2094,
XX PRO2145 OR PRO2198. PRO antagonists can be used to inhibit tumour cell
XX growth. The PRO polypeptides and nucleotides are useful in the
XX treatment, diagnosis and prevention of cancer. The antibodies and other
XX anti-tumour compounds may be used to treat various conditions, including
XX those characterised by overexpression and/or activation of the amplified
XX PRO genes. Exemplary conditions or disorders to be treated with such
XX antibodies and other compounds include benign or malignant tumours
XX (e.g., renal, liver, kidney, bladder, breast, gastric, ovarian,
XX colorectal, prostate, pancreatic, lung, vulva, thyroid, hepatic
XX carcinomas, sarcomas, glioblastomas, and various head and neck tumours),
XX leukaemias and lymphoid malignancies, other disorders such as neuronal,
XX glial, astrocytoma, hypothalamic and other glandular, macrophagal,
XX epithelial, stromal and blastocoele disorders, and inflammatory,
XX angiogenic and immunologic disorders. AAC58242 to AAC58366 represent PCR
XX primers and hybridisation probes used in the isolation of the human PRO

CC sequences. AAC58367 to AAC58396 and AAB24057 to AAB24089 represent human
 CC PRO polynucleotide and protein sequences given in the exemplification of
 CC the present invention.

XX Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;

Query Match 12.8%; Score 296.2; DB 21; Length 1509;

Best Local Similarity 60.7%; Pred. No. 5.8e-72;

Matches 506; Conservative 0; Mismatches 318; Indels 9; Gaps 1;

QY 911 AAGTTTGCCTAGCAGGATATCATGAAAGAGACTGTTACACGATCTTTTGATCTCTATA 970

Db 53 ACCTGTCCTCCAGAGGAGTTCAGAGGAGCTGTTACAGGAGCTGGTCAAGAACTACA 112

QY 971 ATACACTAGAACGTCCTGCTTCTCAATGAATCGGACCGTTTACAAATTAAGCTTTGGTTAA 1030

Db 113 ATCCCTGGAGAGCCGCTGCCAATGACTCGCAACCACTCACCGTCTACTTCTCCCTGA 172

QY 1031 CTTTAATGCAAAATATGATGTGGAGAGAAAAATCAATTTGCTAGTCACTAATGTGTGGT 1090

Db 173 GCCTCTGCAGATCATGGACGTGGATGAGAAGAACCAAGTTTAAACCACCAACATTTGGC 232

QY 1091 TAAACTGGAGTGAAGACATGAATCTCCGCTGGACACCTCCGACTATGGCGGAGTTA 1150

Db 233 TGCAAATGCTTGGACAGACTCATTTTACAGTGAATGTGTCAGATATFCCAGGGGTGA 292

QY 1151 AGGATCTGCGAATACCCCGCATCGCATCGGAGCGGACGCTGCTGATGTACAAACAGTG 1210

Db 293 AGACTGTCTGCTTCCAGATGGCCAGATTTGGAAACCAAGACATTTCTCTATAACAGTG 352

QY 1211 CGGATGAGGATTTGACGGCACTTACAGACGAAACGTTGGTGGCGGAACAACGGTCTGT 1270

Db 353 CTGATGAGCGCTTGGAGCCACATTCACACTAACGTTGGTGAATTCCTCGGGCATT 412

QY 1271 GTCTATACGTTCCGCGGGATCTTCAAGTCGAGCTCAAGATCGACATCACCTGGTGTTC 1330

Db 413 GCCAGTACCTGCTCCAGGATATTCAGAGTTCTCTGCTACATCGATGACGTGGTTC 472

QY 1331 CTTTCGATGACCGGCTGGAGATGAAGTTCCGCACTTGGACCTACGACGATTCACG 1390

Db 473 CTTTGTATGTCAGCACTGCAAACTGAAGTTTGGTCTCTGCTTACGGAGGCTGGTCT 532

QY 1391 TGGATTTACAATTTACAAGATGAACCTGGCGGTGATATCAGCAGTACGCTCAACGGCG 1450

Db 533 TGGATCTGCAGATGCAGAGGCA-----GATATCAGTGGCTATATCCCAATGGAG 583

QY 1451 AGTGGGAACCTACTGGGTGTCGCGGCAACGTAACGAGATCTATTACAACCTGTGCCCGG 1510

Db 584 AATGGGACCTAGTGGGAATCCCGGCAAGAGAGTGAAGGTTCTATGATGCTGCAAG 643

QY 1511 AACCTATATAGACATCACCTTCGCCATCATCATFCCCGGACGAACTGTACTATTCT 1570

Db 644 AGCCCTACCCGATGTACCTTTCACAGTACCATTGCGCCGCGCAGGACGCTTACTATGGCC 703

QY 1571 TCACCTGATCATACCTTTGTACTGATTTGCTCCATCGGCTTGTCTCGGATTCACCTGC 1630

Db 704 TCACCTGCTGATCCCTGCTGTGCTCATCTCCGCGCTCGCCCTGCTGGTGTCTCTGCTTC 763

QY 1631 CGCCAGATTCGGGTGAATAATATTCGCTGGGTGTTACCATCTGCTCTCGTGCACCGTGT 1690

Db 764 CTGAGATTCGGGGGGAAGATTTCCCTGGGATTAACAGCTTACTCTCTCTTACCGTCT 823

QY 1691 TTCTGAATATGTTTCCGAGACAATGCCGGCTACTTCCGATGCGGTGCCATTG 1743

Db 824 TCATGCTGCTGCTGAGATCATGCCGCAACATCCGATTCGTTCCGTACCATTTG 876

RESULT 11

AAC90380

ID AAC90380 standard; cDNA: 1509 BP.

XX

AC AAC90380;

XX

DT 14-MAR-2001 (first entry)

XX Wild-type human alpha7 ligand gated ion channel coding sequence.

XX Human; alpha7 nicotinic acetylcholine gated ion channel;

KW 5-hydroxytryptamine; 5-HT3; calcium ion conductance; ss.

OS Homo sapiens.

XX WO200073431-A2.

XX 07-DEC-2000.

XX 25-MAY-2000; 2000WO-US11862.

XX 27-MAY-1999; 99US-0136174.

XX (PHAA) PHARMACIA & UPJOHN CO.

XX Groppi VE, Wolfe ML, Berkenpas MB;

PI P-PSDB; AAB50012.

XX WPI; 2001-061524/07.

DR Special cell culture medium for treating cells and for inducing

PT mammalian cell lines to conduct calcium ions, comprising specified

PT concentrations of ions of sodium, calcium and potassium at specified pH

XX

XX Example 5; Pages 60-61; 77pp; English.

XX The present sequence is the coding sequence for wild-type human alpha7

CC nicotinic acetylcholine gated ion channel. The human alpha7 ion channel

CC was used in the construction of an alpha7/5-hydroxytryptamine (5-HT3)

CC chimeric ligand gated ion channel (see AAC90382 and AAB50014). The

CC alpha7/5-HT3 chimeric ion channel can be expressed by recombinant cells

CC in the present invention, resulting in preferential calcium ion

CC conductance by the cells.

XX Sequence 1509 BP; 297 A; 451 C; 429 G; 332 T; 0 other;

Query Match 12.8%; Score 296.2; DB 22; Length 1509;

Best Local Similarity 60.7%; Pred. No. 5.8e-72;

Matches 506; Conservative 0; Mismatches 318; Indels 9; Gaps 1;

QY 911 AAGTTTGCCTAGCAGGATATCATGAAAGAGACTGTTACACGATCTTTTGATCTCTATA 970

Db 53 ACCTGTCCTCCAGAGGAGTTCAGAGGAGCTTTTACAGAGGAGCTGGTCAAGAACTACA 112

QY 971 ATACACTAGAACGTCCTGCTTCTCAATGAATCGGACCGTTTACAATTAAGCTTTGGTTAA 1030

Db 113 ATCCCTTGGAGAGCGCGTGGCCAAATGACTCGCAACCACTACCGTCTACTTCTCCCTGA 172

QY 1031 CTTTAATGCAAAATATGATGTGGAGAGAAAAATCAATTTGCTAGTCACTAATGTGTGGT 1090

Db 173 GCCTCTGCAGATCATGGACGTGGATGAGAGAACCAAGTTTAAACCACCAACATTTGGC 232

QY 1091 TAAACTGGAGTGGAGACACATGAATCTCCGCTGGAACACCTCCGACTATGGCGGAGTTA 1150

Db 233 TGCAAATGCTTGGACAGATCACTATTTACAGTGAATGTGTCAAGATATCCAGGGGTGA 292

QY 1151 AGGATCTGCGAATACCCCGCATCGCATCTGGAAGCCGGAGCTGCTGATGTACACAGTG 1210

Db 293 AGACTGTCTGTTTCCAGATGGCCAGATTTGGAACCAACAGACATCTTCTCTATACAGTG 352

QY 1211 CGGATGAGGATTTGACGGCACTTACAGACGAAACGTTGGTGGCGGAACAACACGCTCGT 1270

Db 353 CTGATGAGCGTTTGACGCCACATTCACACTAACGTTGGTGAATTTCTTCTGGGCTT 412

QY 1271 GTCTATACGTTCCCGCGGGATCTTCAAGTCGAGCTGCAAGATGACATCAGTGGTTC 1330

Db 413 GCCAGTACCTGCTCCAGGATATTCAGAGTTCTCTGCTACATCGATGCTAGCTGGTTC 472

[illegible]

QY	1571	TCAACGTGATCATACACCTTGTGTACTGATTCCTCCATGGCTTGCCTCGGATTCACCCCTGC	1630
Db	776	TCAAACCTGCTGATCCCTCTGTGCTCATCTCCGCCCTCGCCCTGCTGGTGTTCCTGCTTC	835
QY	1631	CGCCAGATTCGGGTGAAAAATATTCCTGCTGGGTGTACCATCTTGTGCTCTGCTGACCGTGT	1690
Db	836	CTCAGATTCGGGGGAGAGATTTCCCTGGGGATAACAGTCTTTACTCTCTCTTACCGTCT	895
QY	1691	TTCTGAATATGGTTGCCGAGACAATCCGGCTACTTCCGATGGGTGCCATTG	1743
Db	896	TCATGCTGCTGCTGGCTGAGATCATGCCGCAACATCCGATTCGGTACCATTG	948
RESULT 15			
ID	ABSS54875	standard; cDNA; 1876 BP.	
XX	AC	ABSS54875;	
XX	XX	06-DEC-2002 (first entry)	
XX	XX	Human neuronal nicotinic acetylcholine receptor alpha 7 subunit cDNA.	
DE	XX	Human; neuronal nicotinic acetylcholine receptor; nNACHR; gene; ss;	
KW	XX	ion flux; alpha 7 subunit.	
KW	XX	Homo sapiens.	
OS	XX		
XX	XX	Key Location/Qualifiers	
FH	FT	73..1581	
FT	FT	/*tag= a	
FT	FT	/product= "Human nNACHR alpha 7 subunit"	
XX	XX	US6440681-B1.	
PN	XX	27-AUG-2002.	
XX	XX	07-JUN-1995; 95US-0487596.	
XX	XX	03-APR-1990; 90US-0504455.	
PR	PR	30-NOV-1992; 92US-0938154.	
PR	PR	08-MAR-1993; 93US-0028031.	
PR	PR	08-NOV-1993; 93US-0149503.	
XX	XX	(MERI) MERCK & CO INC.	
XX	XX	PI Elliott KJ, Ellis SB, Harpold MM;	
PI	PI	WPI; 2002-711528/77.	
DR	DR	P-PSDB; ABG70492.	
XX	XX	Identifying antagonists or agonists of human neuronal nicotinic	
PT	PT	acetylcholine receptors, by contacting recombinant cells with test	
PT	PT	compound, and measuring ion flux of cells or binding of compound to	
PT	PT	nNACHR -	
XX	XX	Claim 101; Column 57-60; 56pp; English.	
XX	XX	The invention relates to a method for identifying compounds that are	
CC	CC	antagonists or agonists of human neuronal nicotinic acetylcholine	
CC	CC	receptors (nNACHRs), by contacting recombinant cells with a test	
CC	CC	compound and measuring ion flux, the electrophysiological response of the	
CC	CC	cells or binding of the test compound to the nNACHR. The recombinant	
CC	CC	cells are produced by transfection with a nucleic acid encoding at least	
CC	CC	one human nNACHR (alpha or beta) subunit, such that the cells express an	
CC	CC	nNACHR comprising one human subunit encoded by the transfected nucleic	
CC	CC	acid. This sequence represents cDNA encoding the alpha 7 subunit of the	
CC	CC	human nNACHR polypeptide.	
XX	XX	Sequence 1876 BP; 369 A; 553 C; 530 G; 423 T; 1 other;	
XX	XX	Query Match 12.8%; Score 296.2; DB 24; Length 1876;	

Best Local Similarity 60.7%; Pred. No. 6.5e-72;
Matches 506; Conservative 0; Mismatches 318; Indels 9; Gaps 1;

```
Qy 911 AAGTTTCCTAGCAGGATATCATGAAAGAGACTGTTACAGCATCTTTTGGATCCTTATA 970
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 125 ACGTGTCCCTGCGAAGCGAGTTCCAGAGGAGCTTTACAGGAGCTGCTCAAGAACTACA 184
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 971 ATACACTAGAACGTCCTGTTCTCAATGAATCGGACCGTTTACAATTAAAGCTTTGGTTAA 1030
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 185 ATCCCTTGGAGAGSCCGTGGCCAACTGACTCGCAACCACTCACCGTCTACTTCTCCCTGA 244
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1031 CTTTAATGCAAAATATCGATGTGGACGAGAAAATCAATTCTAGTCACTAAATGTGTGGT 1090
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 245 GCCTCTCTCGAGATCATGACGCTGATGAGAAGAACCAAGTTTAAACCACCAACATTTGCG 304
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1091 TAAACTGGAGTGAAGACATGAATCTCGCTGGACACCTCCGACTATGGCGGAGTTA 1150
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 305 TGCAAATGCTTGGACAGATCACTATTTACAGTGAATGTGTGAGAATATCCAGGGGTGA 364
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1151 AGGATCTGCGAATACCCCGCATCGCATCTGGAAGCCGAGCTGCTGATGTACAACAGTG 1210
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 365 AGACTGTTGCTTTCCAGATGGCCAGATTTGGAAACCAGACATTTCTTCTATAACAGTG 424
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1211 CGGATGAGGATTTGACGGCACCTACCAGAGGACGTGGTGGCGGAACAACGGCTCGT 1270
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 425 CTGATGAGCGCTTTGACGCGCACATTCACACATAACGTGTTGGTGAATTTCTTGGGCATT 484
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1271 GTCATATACGTTCCCGCGGGATCTTCAAGTCGACGTGCAAGATCGACATCACGTGGTTCC 1330
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 485 GCCAGTACCTGCCCTCAGGATATTTCAAGAGTTCCTGCTACATCGATGTACGTGGTTTC 544
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1331 CCTTCGATACCAAGCGGTGGGAGATGAAGTTGCGCAGTTGGACCTACGACGGATTCACG 1390
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 545 CCTTTGATGTGCAGCACTGCAAACTGAAGTTTGGGTCTGCTCTTACGGAGGCTGGTCT 604
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1391 TGGATTTACAAATTACAGATGAACCTGGCGGTGATATCAGCAGTTAGCTCTCAACGGCG 1450
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 605 TGGATCTGCAGATGCAGGAGCA-----GATATCAGTGGCTATATCCCCAATGGAG 655
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1451 AGTGGAACTACTGGGTGTCCCGGCAACGTAACAGAGATCTATTACAACCTGTGCCCGG 1510
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 656 AATGGGACCTAGTGGGAATCCCGGCAAGAGAGTGAAGTTCTATGAGTGTGCTGCAAG 715
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1511 AACCTATATAGATCACTCTGCCATCATCATFCCGCGCAGCAACTGTACTATTCT 1570
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 716 AGCCTACCCCGATGTCACTTACAGTGAACATGCGCCGAGCAGCTCTACTATGGCC 775
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1571 TCAACCTGATCACTGTTGTACTGATTCGCTCCATGGCTTGCCTCGGATTCACCTGC 1630
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 776 TCAACCTGCTGATCCCTCTGTGCTCATCTCCGCCCTCGCCCTGCTGTGTCTCTGCTTC 835
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1631 CGCCAGATTCGGGTGAAAAATTATCGCTGGGTGTTACATCTTGTCTCTCGTACCGTGT 1690
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 836 CTGCAGATTCGGGGAGAGATTTCCCTGGGATAACAGTCTTACTCTCTTACCGTCT 895
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 1691 TCTGAAATATGTTGCCGAGACAATGCCGGCTACTTCCGATGGCGTCCCATTTG 1743
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 896 TCATGCTGCTGCTGGTGAAGATCATGCCCGCAACATCCGATTCGGTACCATTG 948
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Job time : 625.968 secs

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OM nucleic - nucleic search, using sw model

Run on: August 21, 2003, 00:04:15 ; Search time 8610.32 seconds
(without alignments)
10975.350 Million cell updates/sec

Title: US-09-303-232-1_COPY_372_2681
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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19	411.4	17.8	3029	3	AF143847	Heliothis
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ALIGNMENTS

RESULT 1	AX009610	Sequence 1	2886 bp	DNA	linear	PAT 06-SEP-2000
LOCUS	AX009610	Sequence 1	from Patent EP0962528.			
DEFINITION	AX009610					
ACCESSION	AX009610					
VERSION	AX009610.1	GI:9996842				
KEYWORDS						
SOURCE		Drosophila melanogaster (fruit fly)				
ORGANISM		Drosophila melanogaster				
		Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
		Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;				
		Ephydroidea; Drosophilidae; Drosophila.				
REFERENCE		1				
AUTHORS		Adamczewski, M.D., Schulte, T.D. and Oellers, N.D.				
TITLE		Nucleic acids encoding acetylcholin-receptor subunits from insects				

JOURNAL Patent: EP 0962528-A 1 08-DEC-1999;
BAYER AG (DE)
FEATURES Location/Qualifiers
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BASE COUNT 942 a 687 c 640 g 617 t
ORIGIN
Query Match 100.0%; Score 2310; DB 6; Length 2886;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 3
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ACCESSION AF272778
VERSION AF272778.1 GI:20152839
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 2907)
AUTHORS Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
TITLE Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing
JOURNAL Genetics 160 (4), 1519-1533 (2002)
MEDLINE 21969411
PUBMED 11973307
REFERENCE 2 (bases 1 to 2907)
AUTHORS Grauso, M. and Sattelle, D.B.
TITLE Direct Submission
JOURNAL Submitted (27-MAY-2000) Human Anatomy and Genetics, MRC-FGU, University of Oxford, South Park Road, Oxford OX1 3QX, UK
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AY036613 2834 bp mRNA linear INV 30-APR-2002
LOCUS Drosophila melanogaster nicotinic acetylcholine receptor Dalpha5
DEFINITION subunit (nAcRalpha34E) mRNA, nAcRalpha34E-B allele, complete cds,
alternatively spliced.
ACCESSION AY036613
VERSION AY036613.1 GI:20340268
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Prosopliidae; Drosophila.
REFERENCE 1 (bases 1 to 2834)
AUTHORS Grauso,M., Reenan,R.A., Culetto,E. and Sattelle,D.B.
TITLE Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
JOURNAL Genetics 160 (4), 1519-1533 (2002)
MEDLINE 21969411
PUBMED 11973307
REFERENCE 2 (bases 1 to 2834)
AUTHORS Grauso,M. and Sattelle,D.B.
TITLE Direct Submission
JOURNAL MRC-FGU Human Anatomy and Genetics,
Submitted (26-MAY-2001) MRC-FGU Human Anatomy and Genetics,
University of Oxford, South Parks Road, Oxford OX1 3QX, UK
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Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, J.F., An, H., Baldwin, D., Banston, J.V., Besson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferreira, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Haulick, J., Hoskins, R.A., Hostin, D., Howland, T.J., Iqegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Paclet, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Swirskas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Direct Submission
Submitted (30-JUN-2001) Berkeley Drosophila Genome Project, MS
64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,

COMMENT
Sequence submitted by:
Berkeley, CA '94720, US
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA '94720

This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive web site (<http://www.fruitfly.org/sequence/>) or send email to bdq@fruitfly.berkeley.edu.

FEATURES
SOURCE

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Indels 88; Gaps 2;

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VERSION
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SOURCE
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE

AUTHORS

Celtniker, S.E., Adams, M.D., Krommiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banazon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferreira, S., Frise, E., Galie, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J.J., Hoskins, R.A., Hostin, D., Howland, T.J., Iqbalwani, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacle, J.B., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirkas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

TITLE

Sequencing of *Drosophila* chromosome 2L, region 35X-35X

JOURNAL

Unpublished

REFERENCE

AUTHORS

Celtniker, S.E., Adams, M.D., Krommiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., An, H., Baldwin, D., Banazon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champe, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferreira, S., Frise, E., Galie, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J.J., Hoskins, R.A., Hostin, D., Howland, T.J., Iqbalwani, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacle, J.B., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirkas, R., Tector, C., Williams, S.M., Zaveri, J.S., Smith, H.O., Rubin, G.M. and Venter, J.C.

Wei, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattel, B., McIntosh, T.C., McLeod, M.P., McPherson, D., Merkulov, G., Milshina, N.V., Mobarry, C., Morris, J., Moshrefi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, L., Muzny, D.M., Nelson, D.L., Nelson, D.R., Nelson, K.A., Nixon, K., Nusskern, D.R., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puri, V., Reese, M.G., Reinert, K., Remington, K., Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Simpson, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C., Stapleton, M., Strong, R., Sun, E., Svirstas, R., Tector, C., Turner, R., Venter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wasserman, D.A., Weinstock, G.M., Weissbach, J., Williams, S.M., Woodgett, W., Wu, D., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zaveri, J.S., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C.

The genome sequence of *Drosophila melanogaster*
 Science 287 (5461), 2185-2195 (2000)
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 Celisner, S.E., Adams, M.D., Kronmiller, B., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C., Rogers, Y., Banzon, J., An, H., Baldwin, D., Banzon, J., Beeson, K.Y., Busam, D.A., Carlson, J.W., Center, A., Champs, M., Davenport, L.B., Dietz, S.M., Dodson, K., Dorsett, V., Dou, L.E., Doyle, C., Dresnek, D., Farfan, D., Ferreira, S., Frise, E., Galle, R.F., Garg, N.S., George, R.A., Gonzalez, M., Houck, J., Hoskins, R.A., Hostin, D., Howland, T.J., Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattel, B., Moshrefi, A., McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunoo, J., Pacleb, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B., Phouanavong, S., Pittman, G.S., Puri, V., Richards, S., Scheeler, F., Stapleton, M., Strong, R., Svirstas, R., Tector, C., Tyler, D., Williams, S.M., Zaveri, J.S., Smith, H.O., Venter, J.C. and Rubin, G.M.

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 Misra, S., Crosby, M.A., Matthews, B.B., Bayraktaroglu, L., Campbell, K., Hradecky, P., Huang, Y., Kaminker, J.S., Prochnik, S.E., Smith, C.D., Tupy, J.L., Bergman, C.M., Berman, B.P., Carlson, J.W., Celisner, S.E., Clamp, M.E., Drysdale, R.A., Emmert, D., Frise, E., de Grey, A.D.N.J., Harris, N.L., Kronmiller, B., Marshall, B., Millburn, G.H., Richter, J., Russo, S., Searle, S.M.J., Smith, E., Shu, S., Smutniak, F., Whitfield, E.J., Ashburner, M., Gelbart, W.M., Rubin, G.M., Mungall, C.J. and Lewis, S.E.

Annotation of *Drosophila melanogaster* genome
 Unpublished
 4 (bases 1 to 272521)
 Adams, M.D., Celisner, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.

Direct Submission
 Submitted (06-SEP-2002) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
 6 (bases 1 to 272521)
 Rockville, MD 20850, USA

5 (bases 1 to 272521)
 FlyBase
 Direct Submission
 Submitted (23-JAN-2003) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
 On Sep 16, 2002 this sequence version replaced gi:7298121.
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VERSION	HTG.
KEYWORDS	2 of 10
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REFERENCE	2 (bases 1 to 320754) Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Kim,E., Lee,B., Lewis,S., Li,P., Lomtan,M.A., Mazda,P., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacble,J.M., Park,S., Pfaffner,B., Poon,L., Sequeira,H., Sethi,H., Snir,E.,
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PUBMED	
AUTHORS	

SVIRSKAS,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.
Direct Submission
Submitted (08-MAR-2000) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, MS 64-121, Berkeley, CA
94720, USA
On or before Mar 22, 2000 this sequence version replaced
gi:2337897, gi:1945578, gi:2337896, gi:2347073, gi:2337894,
gi:3097819, gi:895619, gi:3097823.
Submitted by the Berkeley Drosophila Genome Project. For more
information, visit the BDP Web site: <http://www.fruitfly.org/> This
is the finished sequence of 3C4-36A7.
The orientation of this sequence along the chromosome is left to
right. This sequence was annotated by Sima Misra
(simaf@fruitfly.berkeley.edu) on behalf of the Berkeley Drosophila
Genome Center. Coding sequences are predicted based on
computational analysis, using both gene and CDS prediction programs
and matches to other sequences. These predictions and matches have
been evaluated by the annotators and may have been refined by hand.
The annotators have also used their judgement about which matches
to include in this record. The annotations on this sequence can be
examined in more detail from
<http://www.fruitfly.org/publications/Adh.html>
The annotation syntax used in this record is documented at
[ftp://ftp.ebi.ac.uk/pub/databases/edgp/sequence_annotation.README.v](ftp://ftp.ebi.ac.uk/pub/databases/edgp/sequence_annotation.README.v1.2)
1.2.

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Db 252435 GCAGCAGCAACGAGCAACAGCGGCACAACGAGCAGCACGCAAATATTAAACGGACTTA 252494
Qy 863 ATAACTCATGTATTTTATTTATGATATATTTGAATTTATCTGCTAAAGTT 915
Db 252495 ATAACTCATGTATTTTATTTATGATATATTTGAATTTATCTGCTAAAGTT 252547

RESULT 10
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LOCUS Drosophila melanogaster mRNA for nicotinic acetylcholine receptor
DEFINITION subunit dalpha7 (nAcRalpha-18C gene).
ACCESSION AJ554210
VERSION AJ554210.1 GI:29466436
KEYWORDS nAcRalpha-18C gene; nicotinic acetylcholine receptor subunit dalpha7.

SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1683)
MILLAR,N.S.
Direct Submission
Submitted (31-MAR-2003) Millar N.S., Department of Pharmacology,
University College London, Gower Street, London, WC1E 6BT, UNITED
KINGDOM

FEATURES source Location/Qualifiers
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BASE COUNT 423 a 401 c 421 g 438 t
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Matches 952; Conservative 0; Mismatches 436; Indels 135; Gaps 4;

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Db 119 GCTGTGGCGCTGGACCACATAGAAGCGGCTACTCCACGCCCTCTCTGGACAACACTAAC 178
Qy 973 ACCTAGAACGTCCTGCTCAATGATCGGACCGGTTACAAATTAAGCTTTGGTTTTTAAT 1032
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Qy	1093	AAACTGGAGTGGAAACACATGAATTCGCTGGACACACCTCCGACATATGGCGAGTTAAG	1152
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DEFINITION	Heliolthis virescens putative nicotinic acetylcholine receptor alpha		
ACCESSION	AF143846		
VERSION	AF143846.1	GI:4895004	
KEYWORDS	Heliolthis virescens (tobacco budworm)		
SOURCE	Heliolthis virescens		
ORGANISM	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Noctuoidea; Noctuidae; Heliolthinae; Heliolthis;		
REFERENCE	Schulte, T., Oellers, N. and Adamczewski, M.		
AUTHORS	putative alpha subunits of insect nicotinic acetylcholine receptors		
TITLE	more similar to vertebrate alpha 7 subunits and C. elegans Ce21		
JOURNAL	than to other insect nicotinic acetylcholine receptor alpha subunits		
REFERENCE	Unpublished		
AUTHORS	Schulte, T., Oellers, N. and Adamczewski, M.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-APR-1999) ZF-BTB, Bayer AG, Bldg. Q 18,, Leverkusen		
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ORIGIN	1 others		

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Qy	2227	AGACTGTGCTTATCATATTTACCAATGTTCCGAATATTAGCCACAATAGCTGACTACTA	2286
Db	1739	AGACTGTGCTTATTTATTTTACCTGTTCACAAATCATCGCCAGCTAGCGTGTCTG	1798
Qy	2287	TCGCGCACCATATTTATTGTCTCG	2310
Db	1799	TCGCGCCACACATCATGCTGTG	1822
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AX009612			
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DEFINITION	Sequence 3 from Patent EP0962528.		
ACCESSION	AX009612		
VERSION	AX009612.1	GI:9996844	
KEYWORDS			
SOURCE	Heliothis virescens (tobacco budworm)		
ORGANISM	Heliothis virescens		
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	Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;		
	Noctuoidea; Noctuidae; Heliothinae; Heliothis.		
REFERENCE			
AUTHORS	Adamczewski,M.D., Schulte,T.D. and Oellers,N.D.		
TITLE	Nucleic acids encoding acetylcholin-receptor subunits from insects		
JOURNAL	Patent: EP 0962528-A 3 08-DEC-1999;		
	BAYER AG (DE)		
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	IYNYCPEPDIITFAVIRRKTYIFNLIVPCVLIASMALLGFTLPPDSGKSLIG		
	VTLISLTVFLNMVAETMPATSDAPLLGTYFNCIMPMVASSVYSTLILNYYHRRHD		
	THEEMIRQCVFLYLPWLMRSPGSAATPPPARVPPDLELRSSKSLANVLID		
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BASE COUNT	893 a 953 c 944 g 910 t		
ORIGIN			
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	Best Local Similarity	62.5%;	Pred. No. 4 1e-129;
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Qy	925	GGATATCATGAAAGAGACTGTTACACAGCTCTTTTGGATCCTTATAATACACTAGAACGT	984

Db 425 GGTACACAGAGAAGCGGTACTGACACACCTATTGGACACCTACAACTACTGGAGAG 484
QY 985 CCCGTTCTCAATGAATCGACCGGTTACAATTAAGCTTTGGTTTAACTTTAATGCAAAAT 1044
Db 485 CCCGTCGTCAACGAGAGACCGCGTGCAGCTCTCTTCGGCTCAGCTCATGAGATC 544
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Db 545 ATCGAGTGTGGACGAGAGAAGAACAGCTTTTAATAACAACATCTGGCTAAACTAGAGTG 604
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RESULT 13
E58347
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

E58347
Nucleic acid encoding insect acetyl choline receptor subunit.
E58347
E58347.1 GI:13019346
JP 2000023680-A/2.
Heliothis virescens (tobacco budworm)
Heliothis virescens
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Heliothinae; Heliothis.
1 (bases 1 to 3701)
Martin, A., Nadja, E. and Thomas, S.
Nucleic acid encoding insect acetyl choline receptor subunit
Patent: JP 2000023680-A 2 25-JAN-2000;
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PN JP 2000023680-A/2
PD 25-JAN-2000
PF 26-APR-1999 JP 1999118159
PR 04-MAY-1998 DE 19819829.9
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C1201/68.
PC G01N33/15, G01N33/50/(C12N1/21, C12R1:19), C12N15/00, C12N5/00 CC

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Drosophila melanogaster nicotinic acetylcholine receptor Dalpha6
subunit variant type I (nAcralpha-30D) mRNA, complete cds,
alternatively spliced.

AF321445
AF321445.1 GI:20152844

Drosophila melanogaster (fruit fly)
Drosophila melanogaster
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE
AUTHORS
TITLE
1 (bases 1 to 2023)
Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes,
Dalpha5, Dalpha6 and Dalpha7, in Drosophila melanogaster Identify a
New and Highly Conserved Target of Adenosine Deaminase Acting on
RNA-Mediated A-to-I Pre-mRNA Editing
Genetics 160 (4), 1519-1533 (2002)

JOURNAL
MEDLINE
21969411
PUBMED
11973307
REFERENCE
2 (bases 1 to 2023)
Grauso, M. and Sattelle, D.B.
Direct Submission
Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional
Genetics Unit, University of Oxford, South Park Road, Oxford OX1
3QX, UK

FEATURES
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variation

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 2023)
AUTHORS Grauso, M., Reenan, R.A., Culetto, E. and Sattelle, D.B.
TITLE Novel Putative Nicotinic Acetylcholine Receptor Subunit Genes, Dalpha5, Dalpha6 and Dalpha7, in *Drosophila melanogaster* Identify a New and Highly Conserved Target of Adenosine Deaminase Acting on RNA-Mediated A-to-I Pre-mRNA Editing

JOURNAL Genetics 160 (4), 1519-1533 (2002)
MEDLINE 21969411
PUBMED 11973307

REFERENCE 2 (bases 1 to 2023)
AUTHORS Grauso, M. and Sattelle, D.B.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2000) Human Anatomy and Genetics-Functional Genetics Unit, University of Oxford, South Park Road, Oxford OX1 3QX, UK

FEATURES

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Location/Qualifiers

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